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BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

Field of the Invention

5 The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

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Background to the Invention

Invasive fungal infections (e.g. *Candida* spp., *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

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These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

25 Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

30 Classical approaches for identifying antifungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

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(57) Title: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a reagent for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. Cells that are either unwanted or potentially harmful to the organism undergo the apoptotic process and show events like cell shrinkage, chromatin condensation, cytoplasmic condensation, digestion of nuclear DNA, loss of mitochondrial membrane potential, plasma membrane blebbing and phagocytosis of the cell debris (Schwartz, *et al.* 1993). The Bcl-2 family of proteins is centrally involved in the control of the programmed cell death process (PCD). Proteins of this group belong either to the inhibitors of cell death (Bcl-2, Bcl-X_L) or to the group of proteins promoting apoptosis (Bax, Bak) (Oliva and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 and Korsmeyer 1994; Knudson and Korsmeyer 1997; Reed *et al.* 1998). The ability of the Bcl-2 family of proteins to regulate life and death of a cell is conserved across evolution. Finding of homologues of PCD regulatory genes in plants and animals suggests the possibility that some functions involved in this process may originally have evolved in unicellular organisms, before a divergent development between the plant and the animal kingdom had happened (Apte *et al.* 1995).

Expression of the pro-apoptotic human or mouse Bax protein in *Saccharomyces cerevisiae* did induce cell death in this budding yeast (Saito *et al.* 1994; Greenhalf *et al.* 1996; Zha *et al.* 1996). It was initially described as a process that resembled autophagy with dissolution of the internal organelles and vacuolisation. The apoptotic features characteristic for multicellular eucaryotic cells like morphological changes in nuclear shape and chromatin condensation, were not observed in this yeast (Zha *et al.* 1996). It was therefore suggested that Bax-induced cell death in *S. cerevisiae* is due to the toxicity of the Bax protein itself, mediated by a hypothetical pore-formation without any involvement of a death program (Muchmore *et al.* 1996). Bax expression in the fission yeast *Schizosaccharomyces pombe* did in contrast show some of the typical apoptotic changes like DNA fragmentation, chromatin condensation, dissolution of the nuclear envelope and cytosolic vacuolisation, suggesting the presence of the evolutionary conserved PCD pathway in this unicellular eucaryote (Ink *et al.* 1997; Jurgensmeyer *et al.* 1997). Since it is very unlikely that species dependent differences in the toxicity of the Bax protein are the reason for this observed difference between the two yeasts, a bona fide cell death pathway may well be present in *S. cerevisiae*.

Recent findings of a yeast mutant in the cell division cycle gene *CDC48* show a number of morphological and molecular features that are considered typical indicators of apoptosis markers in metazoan cells: exposure of phosphatidylserine on the outer leaflet of the cytoplasmic membrane, DNA breakage as well as chromatin condensation and fragmentation, supporting the existence of a basic PCD machinery in this unicellular yeast. This theory was

supported by the analysis of a wild type yeast cell expressing the human Bax protein. Comprehensive tests for morphological markers of apoptosis did show a series of changes, identical to morphological markers defining apoptosis (Ligr, Madeo *et al.* 1998). Recent findings from the same group (Madeo *et al.*, 1999) implicate oxygen stress as a general regulator of apoptosis in yeast but the actual mechanism of Bax lethality in *S. cerevisiae* remains unclear. It is an aim of the present invention to provide new bax sequences for expression in yeast and fungi and tools for identifying yeast and candida functions in the pathways leading to programmed cell death.

It is an aim of the present invention to provide nucleic acids as well as polypeptides which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungal infections.

It is a further aim of the present invention to provide uses of these nucleic acid and polypeptide molecules for treating diseases associated with yeast or fungi or for the preparation of (e) medicament(s) for treating said diseases.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicament for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds or polypeptides capable of inhibiting or activating expression of the polypeptides of the invention or capable of selectively modulating expression or functionality of such polypeptides. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds or polypeptides.

It is also an aim of the invention to provide methods for preventing infection with yeast or fungi. It is a further aim of the invention to provide human homologues for the nucleic acids and polypeptides of the invention for use in treating proliferative disorders, such as cancer, or for the prevention of apoptosis in certain diseases, or for the preparation of a medicament for treating such disorders or diseases.

All the aims of the present invention have been met by the embodiments as set out below.

Summary of the invention

Since it has been discovered that the mammalian bax gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes. Identification of genes involved in this process could be important for the development of new antifungal therapeutics.

The present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic BAX gene which could be adequately expressed in this pathogenic organism.

Furthermore, the present inventors identified a range of specific nucleic acids which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. Genes which were differentially expressed (analysed using the Pathways™ software) at different time points after Bax expression are envisaged as candidate genes in the present invention.

Additionally, the invention also relates to *Candida* spp. homologues of the *S. cerevisiae* candidate genes and their uses in stimulating or preventing cell death in yeast and fungi, especially pathogenic yeast and fungi are herewith envisaged.

Furthermore, also part of the invention are the human homologues of these apoptosis-associated *S. cerevisiae* nucleic acids and polypeptides and their potential use in treating proliferative disorders in human and other mammals.

Detailed description of the invention

The present invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248,

250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to e); and

(g) the complement of any of the nucleic acids as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1994), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The expression "functional fragment of a nucleic acid" as used herein means the minimal nucleic acid which is necessary to encode a functional protein (or polypeptide). For instance, in situations where a nucleic acid is provided comprising at the 5' end and at the 3' end more nucleotides than the actual open reading frame, the invention also relates to fragments of the nucleic acid which are smaller but which still contain the workable open reading frame. Also meant are parts of the open reading frame encoding a polypeptide having the same properties as the polypeptide encoded by the complete open reading frame.

The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol. The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,

127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 718, 720, 722, 724, 726, 728, 730 and 732.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are commonly known as "non-pathogenic". Some examples of specific diseases associated with yeast or fungi are further exemplified.

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377,

379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death. According to a more specific embodiment, these nucleic acid sequences are derived from *Aspergillus fumigatus*.

In a more specific embodiment the invention relates to a nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi

selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional

equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586,

588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412,

414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731;

(e) a nucleic acid which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NO 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613,

615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and,

(g) the complement of any of the nucleic acids as specified in a) to f).

In a preferred embodiment the invention relates to nucleic acids from *Candida albicans*, as represented by the SEQ ID NOs 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731.

In an even more preferred embodiment the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid corresponds to a mammal or human homologue of at least one of the sequences represented in SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657,

659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731.

Therefore, according to a further preferred embodiment, the invention relates to an isolated nucleic acid from mammal or human origin which nucleic acid sequence is selected from:

- 5 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - 10 (b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
 - 15 (c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686;
 - 20 (d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
 - 25 (e) a nucleic acid which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 675, 677, 679, 681, 683 and 685;
 - 30 (f) a nucleic acid encoding a functional fragment of any of the nucleic acids as specified in a) to f), (g) the complement of any of the nucleic acids as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- The invention also relates to the use of said nucleic acids for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.
- The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

It should be clear that the invention also relates to all nucleic acids according to the invention and which are specifically described above, and which can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U. A nucleic acid according to the invention may also comprise any modified nucleotide known in the art.

The term "nucleic acid sequence" also includes the complementary sequence to any single stranded sequence given.

According to the invention, these sequences and their homologues in other yeast and fungi or in human or other mammals as well as the polypeptides which they encode represent novel molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides. Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*, such as, but not limited to:

- Candidiasis, caused by *C. albicans* and other members of the genus *Candida*, which are primary or secondary mycotic infections, also named candidosis, moniliasis and thrush;
- Aspergillosis, caused by members of the genus *Aspergillus*, form a spectrum of diseases;
- Histoplasmosis, caused by *Histoplasma capsulatum*, which is a pulmonary disease always seen in HIV positive or other immunocompromised individuals;
- Paracoccidioidomycosis, caused by *Paracoccidioides brasiliensis*, which is a granulomatous disease that originates as a pulmonary disease;
- Blastomycosis, caused by *Blastomyces dermatitidis*, which may be a benign and self-limiting infection or a chronic granulomatous and suppurative mycosis, also named Chicago disease or Gilchrist's disease;
- Coccidioidomycosis, caused by *Coccidioides immitis*, and which is a respiratory infection that typically resolves rapidly, but the mycosis can become acute, chronic, severe or fatal; also named San Joaquin Valley fever or Valley fever;
- Cryptococcosis, caused by *Cryptococcus neoformans*, which is a chronic, subacute to acute pulmonary, systemic or meningitic disease, also named Torulosis;

- Sporotrichosis, caused by *Sporothrix schenckii*, which is a chronic infection characterized by nodular lesions of cutaneous or subcutaneous tissues and adjacent lymphatics that suppurate, ulcerate and drain.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore the invention also relates to the potential use of homologous sequences from human or mammalian origin for preventing and/or alleviating diseases or conditions where apoptosis or non-apoptosis of cells is impaired, for instance in proliferative disorders. In this respect also cancer can be seen as a proliferative disorder. Furthermore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art (Sambrook *et al.*, 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The present invention further relates to a nucleic acid capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof. The term "selectively hybridising" or "specifically hybridising" means hybridising under the conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook *et al.*, 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The invention also relates to an isolated nucleic acid comprising a human homologue of at least one of the yeast or candida nucleic acids described earlier. The invention also relates to a polypeptide encodable by said human homologue of said nucleic acid.

In a further embodiment the invention also relates to an expression vector comprising a human homologue of at least one of the yeast or candida nucleic acids described herein. Said expression vector according can be an expression vector, wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or

eukaryotic host cells. According to a further embodiment, the expression vector comprises an inducible promoter and/or a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

5 According to a preferred embodiment, the invention relates to an antisense version of any of the nucleic acids of the invention and described above.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid capable of selectively hybridising to at least one of the nucleic acids of the invention. In an interesting embodiment the invention relates to a nucleic acid capable of selectively hybridising to a human homologue of at least one yeast or candida nucleic acid described herein.

10 Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid molecules of at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

20 The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

25 According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

30 Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be cloned, bringing the primers into

contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. Said promoter may be either constitutive, inducible or cell- or tissue- or organ-specific. The expression vector may advantageously be a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin, or any other host wherein said vector can be introduced by at least one of the methods known in the art. However, preferred host cells are lower eukaryotic cells such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

25 In a further embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

30 The invention further relates to any one of the nucleic acids as defined above for use as a medicament.

Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides,

leading to impaired growth or death of yeast and fungi with reductions of associated illnesses or diseases.

Also envisaged in the present invention are promoter or other control sequences that are comprised within the nucleic acids of the invention, said nucleic acid control sequences can also serve as a target for the identification of compounds or proteins which interfere with the control of expression of downstream encoded polypeptides.

Furthermore, also the human homologues of the yeast and candida nucleic acids may be useful in diseases where apoptosis of cells plays a substantial role, both in situations where apoptosis of (particular) cells is wanted or unwanted.

The invention thus also relates to the use of any of the nucleic acids of the invention or to a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases. As described above, the invention also relates to the use of antisense molecules of the nucleic acids of the invention or to an antisense of any of the human homologues for treating proliferative disorders or for the prevention of apoptosis in certain disorders or diseases.

Said nucleic acids, human homologues and antisense molecules can also be used for the preparation of a medicament for treating or preventing the above-mentioned diseases.

According to yet another embodiment, the invention relates to at least one polypeptide encodable by a nucleic acid of the invention.

The invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein.

(b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54,

56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,
(d) a functional fragment of any of said proteins as defined in a) to c).

20 (d) a functional fragment of any of said proteins as defined in a) to c),
for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide

scanning techniques as described in Geysen *et al.* (1986). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75, 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50,

52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000.

178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,

254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320

358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414 and 416. Also according to the

invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 398-400, 402-404, 406-408, 410-412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432.

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508,

510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574,

576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650,

652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and the use of human polypeptides as represented by SEQ ID NOs 676, 678, 680 and 682.

680, 682, 684 and 686.

Thus, according to a preferred embodiment, the present invention relates to an isolated

polypeptide which is involved in a pathway for programmed cell death of yeast or fungi, for instance a *Candida* spp., selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOS 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430,

432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498,

500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730, 732, 734, 736, 738, 740, 742, 744, 746, 748, 750, 752, 754, 756, 758, 760, 762, 764, 766, 768, 770, 772, 774, 776, 778, 780, 782, 784, 786, 788, 790, 792, 794, 796, 798, 800, 802, 804, 806, 808, 810, 812, 814, 816, 818, 820, 822, 824, 826, 828, 830, 832, 834, 836, 838, 840, 842, 844, 846, 848, 850, 852, 854, 856, 858, 860, 862, 864, 866, 868, 870, 872, 874, 876, 878, 880, 882, 884, 886, 888, 890, 892, 894, 896, 898, 900, 902, 904, 906, 908, 910, 912, 914, 916, 918, 920, 922, 924, 926, 928, 930, 932, 934, 936, 938, 940, 942, 944, 946, 948, 950, 952, 954, 956, 958, 960, 962, 964, 966, 968, 970, 972, 974, 976, 978, 980, 982, 984, 986, 988, 990, 992, 994, 996, 998, 1000, 1002, 1004, 1006, 1008, 1010, 1012, 1014, 1016, 1018, 1020, 1022, 1024, 1026, 1028, 1030, 1032, 1034, 1036, 1038, 1040, 1042, 1044, 1046, 1048, 1050, 1052, 1054, 1056, 1058, 1060, 1062, 1064, 1066, 1068, 1070, 1072, 1074, 1076, 1078, 1080, 1082, 1084, 1086, 1088, 1090, 1092, 1094, 1096, 1098, 1100, 1102, 1104, 1106, 1108, 1110, 1112, 1114, 1116, 1118, 1120, 1122, 1124, 1126, 1128, 1130, 1132, 1134, 1136, 1138, 1140, 1142, 1144, 1146, 1148, 1150, 1152, 1154, 1156, 1158, 1160, 1162, 1164, 1166, 1168, 1170, 1172, 1174, 1176, 1178, 1180, 1182, 1184, 1186, 1188, 1190, 1192, 1194, 1196, 1198, 1200, 1202, 1204, 1206, 1208, 1210, 1212, 1214, 1216, 1218, 1220, 1222, 1224, 1226, 1228, 1230, 1232, 1234, 1236, 1238, 1240, 1242, 1244, 1246, 1248, 1250, 1252, 1254, 1256, 1258, 1260, 1262, 1264, 1266, 1268, 1270, 1272, 1274, 1276, 1278, 1280, 1282, 1284, 1286, 1288, 1290, 1292, 1294, 1296, 1298, 1300, 1302, 1304, 1306, 1308, 1310, 1312, 1314, 1316, 1318, 1320, 1322, 1324, 1326, 1328, 1330, 1332, 1334, 1336, 1338, 1340, 1342, 1344, 1346, 1348, 1350, 1352, 1354, 1356, 1358, 1360, 1362, 1364, 1366, 1368, 1370, 1372, 1374, 1376, 1378, 1380, 1382, 1384, 1386, 1388, 1390, 1392, 1394, 1396, 1398, 1400, 1402, 1404, 1406, 1408, 1410, 1412, 1414, 1416, 1418, 1420, 1422, 1424, 1426, 1428, 1430, 1432, 1434, 1436, 1438, 1440, 1442, 1444, 1446, 1448, 1450, 1452, 1454, 1456, 1458, 1460, 1462, 1464, 1466, 1468, 1470, 1472, 1474, 1476, 1478, 1480, 1482, 1484, 1486, 1488, 1490, 1492, 1494, 1496, 1498, 1500, 1502, 1504, 1506, 1508, 1510, 1512, 1514, 1516, 1518, 1520, 1522, 1524, 1526, 1528, 1530, 1532, 1534, 1536, 1538, 1540, 1542, 1544, 1546, 1548, 1550, 1552, 1554, 1556, 1558, 1560, 1562, 1564, 1566, 1568, 1570, 1572, 1574, 1576, 1578, 1580, 1582, 1584, 1586, 1588, 1590, 1592, 1594, 1596, 1598, 1600, 1602, 1604, 1606, 1608, 1610, 1612, 1614, 1616, 1618, 1620, 1622, 1624, 1626, 1628, 1630, 1632, 1634, 1636, 1638, 1640, 1642, 1644, 1646, 1648, 1650, 1652, 1654, 1656, 1658, 1660, 1662, 1664, 1666, 1668, 1670, 1672, 1674, 1676, 1678, 1680, 1682, 1684, 1686, 1688, 1690, 1692, 1694, 1696, 1698, 1700, 1702, 1704, 1706, 1708, 1710, 1712, 1714, 1716, 1718, 1720, 1722, 1724, 1726, 1728, 1730, 1732, 1734, 1736, 1738, 1740, 1742, 1744, 1746, 1748, 1750, 1752, 1754, 1756, 1758, 1760, 1762, 1764, 1766, 1768, 1770, 1772, 1774, 1776, 1778, 1780, 1782, 1784, 1786, 1788, 1790, 1792, 1794, 1796, 1798, 1800, 1802, 1804, 1806, 1808, 1810, 1812, 1814, 1816, 1818, 1820, 1822, 1824, 1826, 1828, 1830, 1832, 1834, 1836, 1838, 1840, 1842, 1844, 1846, 1848, 1850, 1852, 1854, 1856, 1858, 1860, 1862, 1864, 1866, 1868, 1870, 1872, 1874, 1876, 1878, 1880, 1882, 1884, 1886, 1888, 1890, 1892, 1894, 1896, 1898, 1900, 1902, 1904, 1906, 1908, 1910, 1912, 1914, 1916, 1918, 1920, 1922, 1924, 1926, 1928, 1930, 1932, 1934, 1936, 1938, 1940, 1942, 1944, 1946,

568, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590,

592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 676, 678, 680, 682, 684, 686, 688, 690, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732.

20 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and

30 (d) a functional fragment of any of said polypeptides as defined in a) to c).

According to a further preferred embodiment, the present invention relates to an isolated polypeptide which is involved in a pathway for programmed cell death of mammalian cells selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 676, 678, 680, 682, 684 and 686, or encoding a functional equivalent, derivative or bioprecursor of said protein;

5 (b) a polypeptide having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences as represented by any of SEQ ID NOs human 676, 678, 680, 682, 684 and 686;

10 (c) a polypeptide having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 676, 678, 680, 682, 684 and 686; and,

(d) a functional fragment of any of said polypeptides as defined in a) to c).

15 The invention also relates to the polypeptides of the invention and described above for use as a medicament.

Pharmaceutical or fungicidal compositions comprising at least one of the nucleic acids, antisense molecules, polypeptides of the invention optionally together with a pharmaceutically acceptable carrier, diluent or excipient therefor, are also part of the invention.

20 The polypeptides described above or for the prevention of apoptosis in certain diseases, used for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention furthermore relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof, an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

25 The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative amino acid changes.

30 The present invention also relates to a vaccine for immunizing a mammal comprising at least one (recombinant) nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier. Preferred vaccines are those that can be used for immunization against infections caused by yeast and fungi. Other preferred vaccines can be used for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases.

expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds (or polypeptides) may carry agonistic or antagonistic properties. The compounds (and polypeptides) to be screened may be of extracellular, intracellular, biologic or chemical origin.

Different alternative methods for identification of said compounds or polypeptides form part of the present invention.

According to a specific embodiment the invention relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences of the invention, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth and/or death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and (e) optionally identifying the compound.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

Another alternative to the above described method comprises (a) contacting a compound to be tested with a genetically modified yeast or fungus in which modification results in the

overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus, in addition to contacting wild type cells with said compound, (b) monitoring the growth and/or death rate and/or activity of said genetically modified yeast or fungi cells compared to said wild type cells wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and, (e) optionally identifying the compound.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule of the invention joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound or polypeptide to be tested with at least one of the polypeptides of the invention, (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound or polypeptide being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and (d) optionally identifying the compound or polypeptide.

The invention also relates to a method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of (a) providing a two-hybrid screening system wherein a polypeptide of the invention and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method as described above, are expressed, (b) interacting said compound with the complex formed by the expressed proteins as defined in a), (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and optionally (d) identifying the compound.

According to another embodiment the invention relates to a method for identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises: (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid of the invention joined in frame with a reporter gene, (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and, optionally (c) identifying the compound.

Yet another embodiment of the invention is a method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of: (a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid or by any of the vectors of the invention as a bait and a *S. cerevisiae* cDNA library as a prey are used, (b) detecting an interaction between said polypeptide and a *S. cerevisiae* polypeptide encoded by said cDNA library, and, optionally (c) identifying said *S. cerevisiae* polypeptide.

The term "cells" as used in the above methods relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps: incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter, regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion, detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell, optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. Gal4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of Gal4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of Gal4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are

able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant progress in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are: overlay, ligand blotting,

band-shift, co-immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein targeting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Jersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing and protein translocation.

10 All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to *in vitro* and *in vivo* model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. *In vivo* modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The invention further relates to a method for preparing pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound as identified above

with a suitable pharmaceutically acceptable carrier. The invention also relates to said pharmaceutical composition.

The compounds or pharmaceutical compositions of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections, more preferably where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

10 These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient thereof.

A medicament according to the invention not only relates to fungicidal and fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

15 According to yet another embodiment, the invention relates to a genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids or the polypeptides of the invention, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention, a pharmaceutical composition or a genetically modified organism as described above for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

25 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30 According to a preferred embodiment, the invention relates to a genetically modified mammalian cell or non-human organism as described above wherein said modification comprises the

expression of an antisense molecule to at least one of the nucleic acids of the invention or an antisense molecule to a mammalian homologue of said nucleic acid.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

Some examples of preferred human homologues of yeast and/or *Candida* spp. sequences which can be used in the above methods are represented in SEQ ID NOs 675 to 686.

10 The invention further relates to the compounds identifiable according to the above-described method and their use as a medicament.

The invention further relates to a method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound identifiable according to the above-described methods with a suitable pharmaceutically acceptable carrier.

15 The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

20 Furthermore, the present inventors overexpressed the Bax protein in the pathogenic yeast *Candida albicans* and found that this leads to a similar phenotype. However these results could only be received after having constructed a new synthetic bax gene which could be adequately expressed in this pathogenic organism.

Therefore, the present invention relates to an isolated nucleic acid representing a synthetic

BAX-gene for expression in *Candida* spp. selected from the group of:

- 25 a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
- b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
- c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
- d) a nucleic acid which is more than 75 % identical, preferably more than 80%, 85%, 90% or 95% identical, most preferably more than 97% identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as
- 30 defined in b) or c), and
- e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences.

or a nucleic acid representing the complement of any of said nucleic acids as defined in (e) to (d).

5 The synthetic BAX gene shows 73.7% identity with the gene coding for Bax- α . It should be clear that the present invention also relates to nucleic acids wherein other, also frequently used *Candida* spp. codons, are used instead of the choice made for the sequence represented in SEQ ID NO 1. (Table 8)

It should be clear that all nucleic acids according to the invention and which are specifically described above, can be DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

10 According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a suitable vector, preferably an expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to one or more control sequences allowing the expression in host cells, such as a suitable promoter, or the like, to ensure expression of the proteins according to the invention in a suitable prokaryotic or eukaryotic host cell. In this respect, a constitutive or an inducible promoter can be used.

15 As described in the examples, the invention also relates to nucleic acids and constructs comprising the synthetic BAX, or parts thereof, as a fusion with a carrier gene, such as, but not restricted to the yeast *GFP* gene. It is not necessary to include the complete gene of the fusion partner in the expression construct, so the invention relates to various fusion products which can result from the synthetic BAX gene and its fusion partner.

20 The expression vectors comprising the synthetic construct or fusion protein and the host cell defined herein also form part of the present invention. Said host cell can be from bacterial, yeast, fungal, insect, mammal or human origin. An interesting host cell according to the invention is a *Candida* spp. cell.

25 In another embodiment, the expression vector may further comprise an inducible promoter, and/or further a reporter molecule.

The invention also relates to a vector as described above for inducing programmed cell death in *Candida* spp.

30 The invention further also relates a genetically modified yeast or fungal cell as described above wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

The invention also relates to a genetically modified *Candida* spp. cell wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death

According to a further embodiment, the invention relates to a method for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death using a synthetic BAX gene, as described above, or a vector comprising said gene as described herein, or a genetically modified yeast or fungal cell as described above.

- 5 In this respect different model systems are envisaged. It has been shown in the present invention that expression of the synthetic BAX gene as a fusion protein more rapidly kills the host cells than when expressed without a fusion partner. Accordingly there will be a difference in which *Candida* spp. genes will be differentially expressed in each system. The invention thus relates to methods for identifying genes in *Candida* spp. which are differentially expressed in a pathway eventually leading to programmed cell death, wherein in said methods the host cells will need a longer or shorter time period for starving. Said time period is dependent on the expression construct or system used.

The invention further relates to a method for obtaining and identifying *Candida* spp. sequences (genes or polypeptides) involved in a pathway eventually leading to programmed cell death comprising the steps of:

- a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid as described above or a vector as described above as a bait and a *Candida* spp. cDNA library as a prey are expressed,
- b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
- c) identifying said *Candida* spp. polypeptide.

The invention also relates to a method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:

- a) providing a genetically modified organism as described above,
- b) expressing a cDNA library in said genetically modified organism, and,
- c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.

The invention further relates to a method for identifying Bax-resistant yeast or fungi comprising the steps of:

- a) providing (a) genetically modified yeast or fungi as described above,
- b) treating said genetically modified yeast or fungi with a mutagen,
- c) isolating resistant yeast or fungal cells, and,
- d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.

11

The invention further relates to any of the methods described above wherein said genetically modified organism is a *Candida* spp.

The invention also relates to an isolated *Candida* spp. nucleic acid identifiable by any of the methods described above.

5

The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

Figure 1. *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID NOs 17 to 396 and SEQ ID

5 NOs 691 to 716)

Figure 2. *Candida albicans* (SEQ ID NOs 397 to 674, 687, 688 and 717 to 732) and human homologues (SEQ ID NOs 675 to 686).

Human homologues were confirmed via forward and reverse BLAST using BLOSUM62 as a scoring matrix.

10 **YGL080W** (SEQ ID NO 161) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (390 bp (SEQ ID NO 675), 109 aa (SEQ ID NO 676)) LOC51660/g7706369 has no reported cellular role or biochemical function.

15 **YGR243W** (SEQ ID NO 189) codes for a yeast protein with an unknown cellular role and an unknown biochemical function. The human homologue (384 bp (SEQ ID NO 677), 127 aa (SEQ ID NO 678)) DKFZP564B167/g5817257 has no reported cellular role or biochemical function.

20 **YGR183C (QCR9)** (Table 3) codes for a yeast protein with a known cellular role and a known biochemical function. QCR9 codes for subunit 9 of ubiquinol cytochrome-c reductase (7.3 kDa protein) which is a component of the ubiquinol cytochrome-c reductase complex. Cellular role: energy generation. Biochemical function: oxidoreductase and active transporter. The human homologue (132aa (SEQ ID NO 679), 399bp (SEQ ID NO 680)) AF161536 was predicted to have an analogous cellular role and biochemical function.

25 **YBR009C** (SEQ ID NO 37), **YGR209C** (SEQ ID NO 187) and **YPR028W** (SEQ ID NO 393) correspond to known yeast ORFs. Their human homologues have a reported cellular role or biochemical function.

30 **Figure 3.** Yeast genome microarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters (I and II). Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.

The spots represent the genome wide expression profile without (Minus BAX) and with (Plus BAX) induction of Bax expression for 30 min, 1 hour, 2 hours, 3 hours and 6 hours.

35 **Figure 4.** Yeast cells with a disrupted **YGR183C** gene are fully resistant to Bax-induced cell death. Resistance is observed in both the low-copy (A) and the high-copy (B) Bax

expression system. Clonogenic survival was determined by recovering cells at various times from galactose-containing medium and plating of 1000 cells on glucose-based semisolid medium. Data are representative of three experiments (mean \pm SD, n=3). SD bars are obscured by symbols.

5 **Figure 5.** Scheme for the synthesis of the synthetic BAX gene using *C. albicans* optimal codons.

Figure 6. DNA (SEQ ID NO 1) and protein (SEQ ID NO 2) sequence of the synthetic *C. albicans* BAX gene.

Figure 7. Representation of the expression constructs of the synthetic CaBAX gene (A) and the YEGFP-synth CaBAX fusion (B).

10 **Figure 8.** Growth of the *Candida Albicans* transformants: the individual transformants of pGAL1P:synthCaBAX and pGAL1P:GFP-synthCaBAX were streaked onto plates containing either 2% glucose or 2% galactose as sole carbon source. Growth was monitored 4 days later.

15 **Figure 9.** Growth kinetics of GAL1P:synthCaBAX (A) and GAL1P:GFP-synthCaBAX (B) on galactose containing minimal medium.

20 **Figure 10.** Immunoblot analysis of two independent transformants of GAL1P:synthCaBAX after 15 hours Bax induction on minimal galactose containing media. The arrow at 20kDa indicates the position of the Bax protein. The band seen at 50kDa probably represents a cell wall mannan. Not all of the contamination of the polyclonal Bax antibody could be removed by the treatment with *S. cerevisiae* mannan.

Figure 11. Immunoblot analysis of the GAL1P:GFP-synthCaBAX strain on galactose containing minimal medium. The band appearing at 45kDa represents the Gfp-Bax fusion protein, while the band at 20kDa represents the Gfp protein alone.

25 **Figure 12.** FACS analysis of two independent GAL1P:GFP-synthCaBAX transformants grown on galactose containing media: the light grey peak indicates the autofluorescence of the wt strain, the GFP-fluorescence peak is not shaded.

30 **Figure 13.** Viability test synthCaBAX (A) and GFP-synthCaBAX transformants (B). Cells were pregrown in minimal dextrose medium and then switched to fresh minimal medium containing galactose. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represented the viable fraction of the total pool.

35 **Table 1.** Oligonucleotides used for construction of the synthetic CaBAXx gene: start and stop codon are in bold, restriction sites used for cloning are in bold and italic.

Tables 2-6. Genes modulated by Bax expression in *S. cerevisiae*.

This list includes the genes for which mRNA levels changed significantly after a 30 min (Table 2), 1 hour (Table 3), 2 hours (Table 4), 3 hours (Table 5) or 6 hours (Table 6) induction of Bax protein expression. The Qi values were calculated using the Pathways™ software (Research Genetics).

5

Table 7. Genes modulated by Bax expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly after induction of Bax protein expression. The Qi values were calculated using the Pathways software (Research Genetics). Positive values correspond with upregulated genes. Negative values correspond with downregulated genes. (Comparable with ↑ and ↓ respectively in Tables 2-6).

10

Table 8. Codon usage for the synthetic BAX gene.

Table 9. Regulation of 23 selected "Bax-specific" functions.

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

5 Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was used for the construction and the amplification of plasmids. Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* strain INVSc1 (Invitrogen®, San Diego, CA, USA) was transformed by means of the lithium acetate method (Schleissl and Gietz, 1989) with YipUTyL or YipUTyLMuBax, after linearisation in the Ty

10 δ element (Zhu, 1986).

Cloning of mouse BAX cDNA

Mouse bax cDNA, encoding the mouse Bax-α protein, was cloned by Pfu DNA polymerase (Stratagene®, La Jolla, CA, USA) chain reaction amplification (PCR) from an EL4/13.18 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15

5'-ATGGACGGGTCCGGGAGCAG-3' (SEQ ID NO 689) and
5'-TCAGCCCCATCTCTCCAGATGGTGAG-3' (SEQ ID NO 690).

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to standard procedures (Sambrook J. *et al.*, 1989).

20

Plasmid constructions

The 2μ ori and the *URA3* marker gene were removed from pUT332 (Gaignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII GAL1* promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI FLP* terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that the plasmid YipUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in the *KpnI-AatII*-opened and blunted YipUT resulted in the plasmid YipUTy. Subsequent insertion of the *LEU2* marker gene, as a blunted *BsaAI-BstGI* fragment, in the *BamHI*-opened and blunted YipUTy resulted in the plasmid YipUTyL.

25

Mouse bax cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII* and subcloned into the *XbaI-HindIII*-opened plasmid YipUTyL, obtaining the final expression plasmid YipUTyLMuBax.

30

The plasmid YipUTyLMuBax has been deposited in the BCCM™/LMBP culture collection as pSCTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA). The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

The yeast filters consist of over 6144 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

Results

Induction of *Bax*-expression in yeast cells

A preculture of yeast strain INVSc1 containing YipUTyLMuBax, wherein 5 *Bax* cassettes under the control of the *GAL1* promoter are integrated in the genome near Ty δ elements, was grown overnight in minimal glucose-containing medium in parallel with the yeast strain INVSc1 containing YipUTyL as a control. The precultures were diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium and incubated for an additional period of 30 min, 1 hour, 2 hours, 3 hours or 6 hours.

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genther Corporation Nashville, TN, USA) according to the GenHunter protocol. $1.5 \cdot 10^8$ cells were concentrated in a microfuge tube and 1 ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA degradation. Chloroform (150 μ l) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 μ l RNase free dH_2O .

First strand cDNA synthesis in the presence of $\alpha\text{-}^{32}\text{P}$ dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YipUTyLMuBax or INVSc1 YipUTyL yeast cells and incorporation of $\alpha\text{-}^{32}\text{P}$ dCTP as follows: 2 μ l (1 $\mu\text{g/ml}$) of oligo dT was added to 20 μg of total RNA in a maximal volume of 8 μ l RNase-free dH_2O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

6 μ l 5x concentrated First Strand Buffer (GIBCO-BRL, Paisley, UK)
 1 μ l 0.1 M DTT
 1 μ l RNase Block (40 units/ μ l) (Stratagene)
 1.5 μ l 20 mM dXTP-solution (X = A, G and T) (Amersham Pharmacia biotech Uppsala, Sweden)
 1.5 μ l SuperScript™ Reverse Transcriptase (200 units/ μ l) (GIBCO-BRL)
 10 μ l $\alpha\text{-}^{32}\text{P}$ dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham Pharmacia biotech Uppsala, Sweden).

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place. Unincorporated label was separated from the probe on a Sephadex G-50 column (Amersham Pharmacia biotech Uppsala, Sweden). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was $5 \cdot 10^8$ cpm/ μ g for both the INVSc1 YipUTyL and the INVSc1 YipUTyLMuBax probes.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α -³²P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb™ solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 ml MicroHyb™ solution (42°C) containing 5 µl polydA (1 µg/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0.5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette (Molecular Dynamics, Sunnyvale, CA, USA) with storage phosphor screen. After 4 days of development the screen was scanned at a resolution of 50 µm using the (BioRad, Richmond, CA, USA) Personal FX. The results of these can be seen in Figure 3.

Example 2: Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the Pathways™ software (Research Genetics, Huntsville, AL, USA) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. The genes as well as the factors with which they are up- or down- regulated are listed in the Tables 2 to 6 for each individual time point. An overview of the up and down regulated genes modulated in function of induction of Bax expression for several time points is shown in Table 7. The sequences of these genes and amino acid sequences that they encode are shown in Figure 1.

Example 3. Comparative gene expression analysis upon Bax-induced cell death and H₂O₂-induced cell death

The oxidative H₂O₂-challenge

A preculture of yeast strain INVSc1 containing YipUTyL was grown overnight in minimal glucose-containing medium. The preculture was diluted in 100-ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells were transferred into 100-ml galactose-containing medium supplemented with 0.1 mM H₂O₂, and

incubated for an additional period of 1 hour. This oxidative challenge resulted in the same final toxicity as a 1-hour induction of Bax expression in the same growth conditions.

First strand cDNA synthesis in the presence of α -³²P dCTP

RNA was isolated as mentioned in Example 1. Probes with high specific activity were prepared (detailed in Example 1) by first strand cDNA synthesis using total RNA isolated from INVSc1 YipUTyL-MuBax or INVSc1 YipUTyL (growth conditions as described in Example 1) or oxidatively stressed INVSc1 YipUTyL yeast cells. The specific activity of all probes was 5.10⁸ cpm/µg.

Quantification of Hybridisation Signals

Hybridisation and signal detection as described in Example 1. Conversion of the digital images to a 16 bit TIFF format using the Quantity One program (BioRad, Hercules, CA, USA) preserved image data and was necessary for file import into the Pathways® software (Research Genetics, Huntsville, AL, USA). Pathways® was used for the quantification of hybridisation signals and these signals were normalised against all data points.

Identification of Bax-responsive genes

Pairwise comparisons of the normalised data obtained from INVSc1 YipUTyL-MuBax (B) and INVSc1 YipUTyL (C) revealed differentially expressed genes. To determine the -fold induction or repression, the normalised signal intensity after Bax induction (B) was divided by that before the shock (C). Visual inspection of the hybridisation spots confirmed their selection (replacement).

Identification of Bax-specific genes within the Bax-responsive pool

Pairwise comparisons of the normalised data obtained from INVSc1 YipUTyL-MuBax (B) and INVSc1 YipUTyL (C) at the 1-hour time point revealed differentially expressed genes. Linear ratios (B vs C) were estimated significant when changes were at least two-fold and the normalised signal intensity of one spot was at least tenfold above the average background value. The normalised data of the Bax-responsive genes were compared with data obtained from the H₂O₂-stressed INVSc1 YipUTyL (H). A Bax-responsive (up-regulated/down-regulated) gene was considered to be Bax-specific when the normalised signal intensity after Bax induction was at least twice as high/low as the corresponding intensity after oxidative stress. Visual inspection of the hybridisation spots confirmed their selection. An overview of the Bax-

specific genes for the 1-hour time point is shown in Table 9. The sequences of these genes and amino acid sequences that they encode are shown in Figure 2.

Example 4. Search for homologues in *Candida albicans* and human

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathtoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA). Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix. The sequences of homologues *Candida* spp. and human genes and the corresponding amino acid sequences are shown in Figure 2.

Example 5. Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to the wild type (WT) cell. Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component

which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test compound.

The assay to be set up involves measurement of growth and/or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti-sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

Example 6. Assay for High Throughput screening for drugs

35 μ l minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent, flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems, Helsinki, Finland). A 96-channel pipettor transfers 2.5 μ l of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (Cal-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, Cal-4, the medium is always supplemented with 20 $\mu\text{g/ml}$ uridine. A single colony is scooped up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250,000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20,000 to 50,000 cells/ml. Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (\pm 0.04) is reached.

200 μ l of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μ l total volume. MW96 plates are incubated (static) at 30°C for 48 hours. Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Example 7. Yeast cell viability assay upon induction of Bax expression

Materials and media

Yeast strains were grown under normal conditions on standard media (Sherman *et al.*, 1979). The *Saccharomyces cerevisiae* BY4742 wild type strain and BY4742 with the *YGR183C* gene disruption (EUROSCARF collection) were transformed by means of the lithium acetate method (Schiestl and Gietz, 1989) with the low-copy centromeric pRS415Bax plasmid or pRS415 as a control, or with the high-copy episomal pRS425Bax plasmid or pRS425 as a control.

Plasmid constructions

The Bax expression cassette, a *BsgI*(blunted)-*SapI*(blunted) fragment excised from YipUTyLMuBax containing the *GAL1* promoter, the *bax* cDNA and the *FLP* terminator, was ligated into the *Ecl136II*-opened pRS415 (ATCC 87520) and pRS425 (ATCC 77106) plasmids, obtaining the low-copy centromeric pRS415Bax and the high-copy episomal pRS425Bax expression plasmids.

Results

Single colonies of yeast cells transformed with pRS415 or pRS415Bax or pRS425 or pRS425Bax were grown in 10 ml minimal glucose-containing medium with vigorous aeration at 30°C to an optical density of 1 OD₆₀₀. Cells were pelleted by centrifugation and washed two times with sterile dH₂O before resuspending in 10 ml minimal galactose-containing medium. After culturing for various times at 30°C, the total cell density of the cultures was determined, and 1000 cells were spread on minimal glucose-based semisolid medium, followed by incubation at 30°C for 3 days. The number of colonies on plates from the 0 hr cultures was designated as 100% (Fig. 4).

Example 8. Bax Expression in Candida cells

Strains

The *Candida albicans* strain CA14 (*ura3 Δ*) was used to perform the experiments (Fonzi and Irwin 1993).

E. coli transformations were done using the Top10 strain from Invitrogen (San Diego, CA, USA) (*F'* *mcrA* Δ *mrr-hsdRMS-mcrBC*) \approx 80 *lacZ*DM15 Δ *lacX74* *deoR* *recA1* *araD139* Δ *(ara-leu)*7697 *galJ* *galK* *rpsL* (*Str*^r) *endA1* *nupG*).

Media

Synthetic dextrose media (SD), containing 2% glucose, 1.34% Yeast Nitrogen Base without amino acids and 0.77g/l CSM-ura (Bio 101, Vista, CA, USA) was used to grow the *Candida albicans* transformants. In case of the wild type (CA14), the media was supplemented with

50µg/ml uridine. To prepare plates the media was solidified with 2% agar. Expression of the synthetic BAX gene was performed using 2% galactose as carbon source.

Construction of the codon-optimised BAX gene

Construction of the synthetic BAX gene followed the nomenclature described for *Candida albicans* (Lloyd and Sharp 1992; Brown, *et al.* 1991; <http://alces.med.umn.edu/candida/codons.html>; <http://www.kazusa.or.jp/codon>). To ensure a high expression of the synthetic gene, the subset of 'optimal' codons of highly expressed genes was used to design the synthetic BAX gene.

The synthCaBAX gene was constructed in three parts using eight oligonucleotides (Fig. 5). The sequences of the oligonucleotides are given in Table 7. Primer A1 introduced upstream of the ATG codon a *Pst*I site and a *Bgl*II site. The *Pst*I site was used later on for direct cloning into the *Candida albicans* expression vector, while the *Bgl*II site served as a linker for a *yEGFP* fusion. Primer C2 introduced a *Sma*I site, suitable for cloning into the expression vector.

Fragment A and B were synthesised in two steps: in a first PCR round primer X1 and X2 (X represents A or B, respectively) were used together. The resulting fragment served as a template in a second PCR round together with primers X1 and X3. Fragment C was synthesised in a single PCR round using the primers C1 and C2. Fragment A and B were cloned into the pCR-BluntII-TOPO vector (Stratagene), while fragment C was cloned into the pCR2.1-TOPO vector (Stratagene). All three fragments were sequenced to ensure that no mutation was introduced by the PCR.

Subsequently, fragment A was digested with *Pst*I and *Taq*I, fragment B with *Taq*I and *Bam*HI and fragment C with *Bam*HI and *Sma*I. The three products were cloned in a quadruple ligation into pUC21 digested with *Pst*I and *Sma*I resulting in the plasmid pUC21::synthCandidaBAX. The sequence of the synthetic BAX gene is shown in Figure 6.

Construction of synthetic BAX- and GFP-synthetic BAX expression plasmids

A *Pst*I-*Sma*I fragment containing the ORF of the synthetic BAX gene was cloned into the *Pst*I-*Sma*I digested vector pGAL1ACT1LUC (W. Martinet, EP application nr 99204557.5) resulting in the expression construct pGAL1P::synthCaBAX (Fig. 7A). To facilitate recognition of the AUG codon during formation of initiation complexes a purine base (A) was introduced at position -3 from the AUG codon (Kozak 1981) using the Quick change site directed mutagenesis kit from Stratagene.

The yeast enhanced GFP gene *yEGFP*, (Cormack *et al.* 1997) was amplified by PCR using primer 5'-AACTGCAGATGCTCTAAAGGTGAAGAAATTATTC-3' (SEQ ID NO 11) as upstream primer and primer 5'-GGAAGATCTCTCCCTTTGTACAAATTCATCC ATACC-3' (SEQ ID NO 12) as

downstream primer. The sense primer introduced a *Pst* I site (shown in bold and italic), while the anti-sense primer contained a *Bgl* II linker (shown in bold and italic) for fusion with the synthetic *BAX* gene. After cloning of the *YEGFP* gene into the PCR2.1-TOPO vector (Stratagene), the gene was sequenced to ensure that no mutation was introduced by PCR.

The *YEGFP*-synth *Candida BAX* fusion was created by cloning a *Pst*-*Bgl*II *YEGFP* fragment together with a *Bgl* II-*Sma* I synthetic *Candida BAX* fragment into the *Pst* I-*Sfu* I digested expression vector *pgAL1ACT1LUC*. The obtained *pgAL1P::YEGFP-synthCaBAX* fusion construct (Fig.7B) was sequenced to ensure that no frameshift had occurred.

10 Creation of the synthetic *BAX* expression strains

Transformation of the expression plasmids was performed using a modified procedure (Logghe, unpublished) of the spheroblasting protocol (Herreros *et al.*, 1992). The plasmids were linearised with *Bpu* I 102 I to allow directed integration into the genome at the *GAL1* promoter site. Correct integration was analysed by Southern blotting. Therefore genomic DNA from different transformants was prepared using the Nucleon® extraction and purification kit (Amersham Pharmacia Biotech) and digested with *Xba* I. The *BAX* probe used in the Southern blot was prepared by PCR. The PCR was performed using the *pgAL1P-synthCaBAX* plasmid as template, together with the sense primer 5'-ATGGATGGTCTGTGTAAC-3' (SEQ ID NO 13) and the anti-sense primer 5'-TTAACCAATTTTTCACAGATG-3' (SEQ ID NO 14). Standard PCR conditions were used. For detection of the *YEGFP* a probe was synthesised by PCR using primer 5'-AGAGATCTCGAGGGATCC-3' (SEQ ID NO 15) as sense primer and primer 5'-GCATTATTGTACAATTCATCC-3' (SEQ ID NO 16) as anti-sense primer. Southern blot hybridisation and detection were performed using the AlkPhos DIRECT labelling and detection system (Amersham Pharmacia Biotech) following the instructions of the manufacturer.

25 Western blot analysis

For Western blot analysis cells were pre-grown over night in SD-ura media till late log phase. The cells were harvested by centrifugation, washed twice with water and inoculated in SG-ura to induce *Bax* expression. Induction was performed for 15 hours. Yeast crude extracts were prepared as described before (Sambook, Fritsch *et al.*, 1989). Detection of the *Bax* protein was performed using a polyclonal rabbit anti-mouse /rat *Bax* antibody (Pharmingen). Due to contamination of this antibody with yeast cell wall mannan antibodies, a very high background occurred. This problem could be avoided by pre-incubation of the antibody with 0.5mg/ml purified yeast mannan (Rossanese *et al.*, 1999). Detection of the *Gfp* protein was done using an anti-Gfp monoclonal antibody (Molecular Probes, Eugene, OR, USA).

Growth curves

For growth curves, yeast cells were grown for 24 h in SD-ura medium (supplemented with uridine for the wild type). These cultures were harvested, washed twice with water and inoculated to an OD_{600} of 0.1 into fresh SD-ura or SG-ura media. Growth was monitored in microtitre plates using the Bioscreen C system (LabSystems).

5 Viability tests

Cells were pregrown in minimal dextrose medium to an OD_{600} of 1. After washing the cells twice with water they were switched to minimal medium containing galactose as carbon source. At the time points indicated, samples were taken and equal cell amounts were spread on minimal dextrose plates. The appearing colonies represent the viable fraction of the pool.

Results : Conditional expression of the synthetic *BAX* gene in *Candida albicans*

A cDNA encoding the full-length mouse *Bax* protein was placed under control of the *Candida albicans* *GAL1* promoter allowing for conditional expression when cells are grown in galactose containing media. Initial experiments were performed using the wild type mouse *bax* gene. Expression of this gene did not result in any detectable phenotype, no difference in growth compared to the wild type was observed when cells were grown on galactose containing media (data not shown). This could be due to the non-traditional codon strategy adopted by *Candida albicans* and related species. Analysis of the codons used in the mouse *BAX* gene revealed a for *Candida albicans* not optimal codon usage as found for highly expressed genes in this yeast. To ensure a high expression of the *BAX* gene a codon-adapted, synthetic version of the gene was created using the strategy described above. The synthetic *BAX* gene was fused to the *YEGFP* to allow screening for transformants with a high *YEGFP*-synthCaBAX expression level using FACS technology. The newly obtained plasmids *pgAL1P::synthCaBAX* and *pgAL1::GFP-synthCaBAX* were transformed into the *C. albicans* CA14 strain. Transformants were selected on uridine-free minimal medium. About 25 transformants of each expression construct were chosen and streaked onto minimal dextrose medium (non-inducing conditions) as well as on minimal galactose medium (inducing conditions). After two days incubation at 30°C all transformants did grow on the glucose containing media. When galactose was used as a sole carbon source, most of the transformants did not grow (Fig. 8). Southern blot analysis of the galactose negative transformants revealed that a copy of the synthCaBAX gene had been integrated into the endogenous copy of the *GAL1* promoter. To study differences in growth, the transformants were grown over night in synthetic glucose containing medium. Subsequently, cells were washed with water and switched to fresh medium containing galactose as carbon source. While the wild type strain did grow well on galactose containing media no growth was

observed for the Bax expressing transformants (Fig. 9A and B). Western blot analysis of the synthCaBAX transformants showed accumulation of the Bax protein (15 hours Bax induction, Fig. 10). A similar result was observed when immunoblotting was performed with the GFP-synthCaBAX expressing strains. Here the fusion protein was detected at the expected molecular weight of about 45K under inducing conditions (galactose as carbon source). In addition to the fusion protein a band appeared at the molecular weight of about 20K. This corresponds to the molecular weight of the Gfp protein alone. Addition of a Gfp-expressing strain as a positive control to the western blot did confirm these results. Here the Gfp protein was detected at the same molecular weight as the unexpected band in the GFP-synthCaBAX expressing strain (Fig. 11). This is most probably due to a partly proteolytic degradation of the fusion protein. Analysis of the Gfp-fluorescence using FACS technology showed a high Gfp-fluorescence signal for the transformants expressing the fusion protein (Fig. 12). When cell viability was analysed, different results were obtained for the synthCaBAX strain and the GFP-synthCaBAX strain. The synthCaBAX strain showed quite a rapid decrease in the amount of colony forming units during the first 6 hours of incubation on galactose containing media. Afterwards the process slowed down significantly. This is in contrast to the results obtained for the strain expressing the gfp-synthCabax fusion protein. Here almost all the cells died at a very rapid rate during the first 3 hours of incubation in media containing galactose as sole carbon source. It is possible that the Bax trigger in the synthCabax expressing cells is not strong enough to kill all cells. The cell has enough time to activate a sort of defence mechanism, possibly by proteolytic degradation of the Bax protein. The situation is different for the fusion protein. Gfp is a very stable protein itself. Fusion of the Gfp to another protein could result in a stabilisation of this protein. It would be more resistant to proteolytic degradation. This would explain the situation for the Gfp-Bax fusion. The Gfp-Bax protein is more protected from proteolytic degradation. Like that it is for a longer period present in the cell. The death trigger is herewith stronger, so the cells die faster. The time that the cells have to activate the proteolytic machinery is not sufficient for them to survive.

Table 1:

| | |
|------------------|---------------------------------------------------------------------|
| Sequence 5' → 3' | |
| A1 | AACTGACGAAAGATCTTCATGGATGTTCTGGTGAACAATTGGGTTCTGGTG |
| A2 | TCCAACTCTTCTGAACAATATGAAACCGGTTGCTTTCTTTGTTG (SEQ ID NO 3) |
| A3 | TGAAAGCATCTTGTGTTGTTGTTGCCAAGGTCAATTCTGGGGTTCCACGAC |
| A2 | ATTCTACCGACTCTATCTTGGATGAAACCTTGGCAACAAAGAACGACC (SEQ ID NO 4) |
| A3 | GGAATTCATGACATCAGCATCTTGGCAATTCATGAAATTCGAATTC |
| A3 | ATCACCGAATTCCTTCTCAACATTCAGACAAATTTTGGTAGAAGCATCTTGTG (SEQ ID NO 5) |
| B1 | GGAATTCGCTGATGTCGATACCGATTCTCCAAGAGAGTCTTCTTCAGAGTCG |
| B2 | CTGCTGATATGTTTCGCTGATGTTGTAATTCACACTG (SEQ ID NO 6) |
| B2 | AATCTGGGACTTTGGTGTACACAAGGCTTTCAAGAACCAATTTAGAACGCGAAGTA |
| B3 | GAACAAAGGACGACTCTACCCAGTTGAAGTTACCA (SEQ ID NO 7) |
| B3 | CCACCTTGATCTTGGATCCAGAACCAATCTTCTCTCAAGAAATTCGAAGGTC |
| C1 | CAACCCATGATGGTTCTTGATCAATTCCTGGGACTTTG (SEQ ID NO 8) |
| C1 | ATTGTTGGTCTGGATCCAGATCAAGGTTGGGAAAGGTTTGTTGTTACTT |
| C2 | CGGTACCCCAACCTGGGCAAAACCGTCA (SEQ ID NO 9) |
| C2 | TCCCGGCGGGGATTAACCCATTTTTTCCAGATGGTCAAGAGCGGCTCAAGAC |
| | ACCAGCGACGAAGATGGTGACCGGTTTGGCCAGGTTGGG (SEQ ID NO 10) |

Table 2: Overview of the differentially expressed genes after 30 min Bax expression**Comparison: INVSc1 YipUTL versus INVSc1 YipUTLB**

| Gene | Cellular role | Cell cycle control | ↑ | 2.00 |
|-----------|---------------|--------------------|-----------|------|
| YBR133C | HS17 | 18932.54 | 37877.20 | ↑ |
| YDR233C | MET32 | 17661.13 | 45567.17 | ↑ |
| YBR112C | SSN6 | 26698.87 | 65315.83 | ↑ |
| YDR145W | TAF61 | 38697.96 | 73117.62 | ↑ |
| YBR269W | SNF5 | 33111.77 | 72328.70 | ↑ |
| YDR216W | ADR1 | 30127.45 | 6815.87 | ↓ |
| YEL009C | GCN4 | 16533.78 | 3030.44 | ↓ |
| YBR089C-A | NHP6B | 22698.93 | 6297.49 | ↓ |
| YMR043W | MCN1 | 39141.64 | 84180.45 | ↑ |
| YKR092C | SRP40 | 5955.83 | 18105.82 | ↑ |
| YMR273C | ZDS1 | 14899.61 | 35508.04 | ↑ |
| YPL089C | RLM1 | 34922.81 | 67556.88 | ↑ |
| YOR372C | NDI1 | 20285.12 | 44445.20 | ↑ |
| YPL037C | EGD1 | 30633.33 | 6250.70 | ↓ |
| YBL085W | BOI1 | 7693.28 | 18614.99 | ↑ |
| YBR009C | HHE1 | 16668.00 | 4178.80 | ↓ |
| YNL003W | HHE2 | 48978.04 | 12568.96 | ↓ |
| YDR224C | HTB1 | 67355.40 | 23156.82 | ↓ |
| YBL002W | HTB2 | 25269.02 | 5383.97 | ↓ |
| YER112W | USP1 | 12776.74 | 31470.70 | ↑ |
| YPL190C | NAB3 | 6381.36 | 17892.11 | ↑ |
| YNL112W | DBP2 | 9956.84 | 28036.48 | ↑ |
| YPL078C | ATP4 | 26902.68 | 5960.38 | ↓ |
| YDL004W | ATP16 | 35525.08 | 3004.34 | ↓ |
| YDR037W | ATP17 | 14419.41 | 756.86 | ↓ |
| YDR529C | QCH7 | 35346.95 | 5394.65 | ↓ |
| YGR008C | STF2 | 13275.51 | 2276.27 | ↓ |
| YEL039C | CYC7 | 13604.38 | 2889.66 | ↓ |
| YKL150W | MCN1 | 10537.67 | 30743.75 | ↓ |
| YLR088C | COX12 | 52887.73 | 5455.83 | ↓ |
| YLR327C | | 113.966.77 | 54.014.65 | ↓ |
| YBR149W | ARA1 | 15149.55 | 4095.17 | ↓ |
| YHR094C | HXT1 | 12526.90 | 785.73 | ↓ |
| YDR343C | HXT3 | 36643.13 | 1632.48 | ↓ |
| YDR343C | HXT6 | 77064.71 | 32060.05 | ↓ |
| YDR342C | HXT7 | 76349.13 | 27815.15 | ↓ |
| YER117W | BMH1 | 22856.29 | 44771.71 | ↑ |
| YDR099W | BMH2 | 40127.38 | 74572.38 | ↑ |

| | | | | | |
|----------|--------|----------|-----------|---|-------|
| YGR070W | ROM1 | 12055.28 | 28169.57 | ↑ | 2.34 |
| YGR023W | MRL1 | 7354.78 | 19848.06 | ↑ | 2.67 |
| YGR034W | RPL26B | 71942.46 | 74625.22 | ↑ | 1.04 |
| YLR216C | CPH6 | 9616.80 | 31128.02 | ↑ | 3.24 |
| YFR052W | RPN12 | 5583.57 | 14655.67 | ↑ | 2.66 |
| YDL147W | RPN5 | 31932.20 | 52939.11 | ↑ | 1.66 |
| YGR132C | PHB1 | 15429.56 | 5591.19 | ↓ | 2.76 |
| YGR135W | PRE8 | 39921.63 | 5517.17 | ↓ | 7.24 |
| YFR010W | UBP6 | 1892.76 | 828.84 | ↓ | 2.28 |
| YHR037W | GPX3 | 7868.22 | 21769.00 | ↑ | 2.77 |
| YDR513W | TRR1 | 55986.32 | 33263.12 | ↓ | 1.89 |
| YCL035C | GRX1 | 70248.30 | 10859.97 | ↓ | 6.40 |
| YEL014W | HSP12 | 41689.29 | 18658.48 | ↓ | 2.23 |
| YHR053C | CUP1A | 72852.07 | 43488.52 | ↓ | 1.88 |
| YHR055C | CUP1B | 71834.03 | 56799.80 | ↓ | 2.77 |
| YMR113W | DDR48 | 16670.70 | 5022.40 | ↓ | 3.32 |
| YMR51W-A | HOR7 | 26676.95 | 417.36 | ↓ | 64.1 |
| YLR043C | TRX1 | 58251.39 | 4455.79 | ↓ | 13.13 |
| YBL064C | PRX1 | 21525.00 | 40865.00 | ↑ | 1.80 |
| YOL151W | GHE2 | 2824.55 | 24152.03 | ↑ | 9.20 |
| YBL081W | | 73834.11 | 74612.35 | ↑ | 1.01 |
| YDR366C | | 39998.46 | 57428.80 | ↑ | 1.44 |
| YCR004C | YCP4 | 6869.06 | 28115.73 | ↑ | 4.09 |
| YCR013C | | 3986.55 | 15144.34 | ↑ | 3.80 |
| YBR050C | REG2 | 4687.91 | 14408.20 | ↑ | 3.07 |
| YBL109W | | 18744.60 | 35440.24 | ↑ | 1.89 |
| YDR154C | | 19565.23 | 68428.03 | ↑ | 3.55 |
| YEL071W | DLD3 | 22235.73 | 68790.83 | ↑ | 3.09 |
| YHR065W | | 14426.76 | 34898.68 | ↑ | 2.42 |
| YGR069W | | 43413.57 | 72420.39 | ↑ | 1.67 |
| YDR544C | | 13567.00 | 27004.37 | ↑ | 1.99 |
| YGR236C | | 24927.59 | 8032.35 | ↓ | 3.10 |
| YIL057C | | 24246.39 | 773.56 | ↓ | 31.34 |
| YGL080W | | 23425.00 | 3217.81 | ↓ | 7.28 |
| YGL072C | | 18437.52 | 2652.80 | ↓ | 6.20 |
| YHR066C | RSC30 | 72072.88 | 57446.85 | ↓ | 1.25 |
| YKL054C | VID31 | 17590.49 | 38258.80 | ↑ | 2.13 |
| YLR131C | | 7892.40 | 24164.87 | ↑ | 3.02 |
| YJRI15W | | 64690.69 | 102066.34 | ↑ | 1.58 |
| YJL188C | BUD19 | 7580.28 | 22325.70 | ↑ | 2.95 |
| YKR040C | | 50934.78 | 100733.41 | ↑ | 1.98 |
| YLR053C | | 8117.66 | 20317.34 | ↑ | 2.50 |
| YOR121C | | 59950.94 | 92470.43 | ↑ | 1.54 |
| YNL143C | | 98811.28 | 110534.34 | ↑ | 1.12 |
| YOR131C | | 7841.55 | 22553.72 | ↑ | 2.81 |
| YNL38W | | 21800.45 | 38177.28 | ↑ | 1.78 |
| YNL179C | | 13729.36 | 39516.53 | ↑ | 2.88 |
| YOL150C | | 3408.74 | 60298.39 | ↑ | 17.89 |

| | | | | | |
|-----------------------------------------|----------|-----------|-----------|------|-------|
| YMR107W | 65118.70 | 10042.46 | ↓ | 6.48 | |
| YKL065C | YET1 | 89556.19 | 12804.88 | ↓ | 5.43 |
| YJR096W | | 21780.37 | 10655.13 | ↓ | 2.04 |
| YJL161W | | 16468.73 | 2618.26 | ↓ | 6.29 |
| YML128C | MSC1 | 80130.20 | 13795.84 | ↓ | 5.81 |
| YMR251W | | 28879.95 | 417.38 | ↓ | 64.41 |
| YMR173W-A | | 110104.98 | 61951.23 | ↓ | 1.78 |
| YPL201C | | 17913.32 | 5018.97 | ↓ | 3.57 |
| YOR285W | | 64074.73 | 29749.43 | ↓ | 2.15 |
| YOR286W | | 13458.08 | 733.08 | ↓ | 18.36 |
| Cellular role: Cell wall maintenance | | | | | |
| YKR076W | ECM4 | 2674.15 | 13040.04 | ↑ | 4.88 |
| YLR390W | ECM19 | 5472.05 | 15145.85 | ↑ | 2.77 |
| Cellular role: Membrane fusion | | | | | |
| YHR138C | | 18921.35 | 3707.57 | ↓ | 5.37 |
| Cellular role: Vesicular transport | | | | | |
| YHR161C | YAP180A | 13086.35 | 30160.90 | ↑ | 2.30 |
| YPL065W | SEC16 | 6968.57 | 15208.49 | ↑ | 2.28 |
| YKL196C | YK16 | 18933.84 | 2890.07 | ↓ | 6.55 |
| YPR029W | YIP2 | 25434.34 | 2049.47 | ↓ | 12.41 |
| Cellular role: DNA repair/recombination | | | | | |
| YDL059C | RAD59 | 1948.61 | 13089.13 | ↑ | 6.72 |
| Cellular role: DNA synthesis | | | | | |
| YEL032W | MCH3 | 23422.85 | 44327.48 | ↑ | 1.89 |
| Cellular role: Amino acid metabolism | | | | | |
| YIL074C | SER33 | 3978.42 | 16702.66 | ↑ | 4.20 |
| YGR155W | CYS4 | 4184.59 | 19270.89 | ↑ | 4.61 |
| Cellular role: Fatty acid metabolism | | | | | |
| YHR179W | OYE2 | 2291.36 | 40274.02 | ↑ | 17.58 |
| Cellular role: Protein translocation | | | | | |
| YNL131W | TOM22 | 16287.21 | 1679.78 | ↓ | 9.70 |
| Cellular role: Small molecule transport | | | | | |
| YDR276C | SNA1 | 21148.46 | 1580.68 | ↓ | 13.38 |
| YOR267C | HRK1 | 62689.30 | 110516.24 | ↑ | 1.76 |
| YHR039-C | VMA10 | 60107.90 | 8490.93 | ↓ | 7.08 |
| YOR382W | FIT2 | 6780.82 | 27236.15 | ↑ | 4.02 |

Table 3: Overview of the differentially expressed genes after 1h Box expression
Comparison: INVSc1 YipUTL versus INVSc1 YipUTyLB

| Gene | Gene | Normalized Expression | Δ value | Category |
|-------------------------------------------------|---------|-----------------------|-----------|----------|
| Cellular role : Polymerase II transcription | | | | |
| YDR145W | TAF61 | 20729.58 | 57376.27 | ↑ 2.77 |
| YDR216W | ADR1 | 5925.91 | 18459.00 | ↑ 3.11 |
| YBR112C | CYC8 | 50188.77 | 84511.50 | ↑ 1.29 |
| YMR043W | MCM1 | 21011.54 | 53700.49 | ↑ 2.56 |
| YPL089C | RLM1 | 23440.54 | 84284.32 | ↑ 2.74 |
| YOR372C | NDI1 | 28412.58 | 50804.99 | ↑ 1.92 |
| Cellular role : Cell cycle control | | | | |
| YBR139C | HSL7 | 18761.64 | 53238.88 | ↑ 2.84 |
| Cellular role : Cell polarity | | | | |
| YBL085W | BOI1 | 37895.40 | 57761.52 | ↑ 1.52 |
| Cellular role : Chromatin structure | | | | |
| YDR224C | HTB1 | 13681.40 | 55656.34 | ↑ 4.07 |
| Cellular role: Energy generation | | | | |
| YGR183C | QCR9 | 23181.54 | 81865.40 | ↑ 3.53 |
| YLR294C | MCR1 | 5054.57 | 28994.72 | ↑ 5.74 |
| YKL150W | MCF1 | 43863.07 | 60593.16 | ↑ 1.39 |
| YMR256C | COX7 | 7608.58 | 28801.54 | ↑ 3.79 |
| YOL126C | MDH2 | 34144.61 | 65326.97 | ↑ 1.81 |
| YLR327C | | 97415.94 | 101651.17 | ↑ 1.04 |
| Cellular role: Vesicular transport | | | | |
| YHR161C | YAP180A | 11602.81 | 34695.20 | ↑ 2.89 |
| YLR206W | ENT2 | 14439.24 | 34621.70 | ↑ 2.40 |
| Cellular role: Carbohydrate metabolism | | | | |
| YDR342C | HXT7 | 65273.56 | 22231.08 | ↓ 2.94 |
| YDR343C | HXT6 | 43572.28 | 6075.38 | ↓ 7.17 |
| YDR345C | HXT3 | 76352.52 | 40298.00 | ↓ 1.89 |
| YGR192C | TDH3 | 38472.30 | 14145.84 | ↓ 2.72 |
| YKR097W | PCK1 | 22919.81 | 38225.98 | ↑ 1.67 |
| YOR374W | ALD4 | 33711.37 | 2607.43 | ↓ 12.83 |
| Cellular role: Signal transduction | | | | |
| YER177W | BMH1 | 16298.14 | 31748.91 | ↑ 1.95 |
| YDR099W | BMH2 | 50572.45 | 65123.58 | ↑ 1.29 |
| Cellular role: Cell wall maintenance | | | | |
| YLR110C | CCW12 | 102525.28 | 11230.41 | ↓ 9.13 |
| Cellular role: Protein modification/degradation | | | | |
| YOR261C | RPN8 | 12575.49 | 32568.47 | ↑ 2.59 |
| Cellular role: Cell stress | | | | |
| YHR053C | CUP1A | 32531.53 | 83579.94 | ↑ 1.95 |
| YHR055C | CUP1B | 27839.82 | 65142.82 | ↑ 2.33 |
| YMR173W | DDR48 | 38338.83 | 60514.70 | ↑ 1.58 |
| YOR031W | CRS5 | 2922.32 | 23848.60 | ↑ 8.16 |

| YLR109W | AHP1 | 43067.08 | 6302.46 | ↓ | 6.53 |
|-----------------------------------------|-------|----------|----------|---|------|
| Cellular role: Unknown | | | | | |
| YBL081W | | 82476.13 | 44279.86 | ↑ | 1.86 |
| YBL109W | | 22988.63 | 63428.23 | ↑ | 2.76 |
| YDR366C | | 14599.17 | 46494.73 | ↑ | 3.18 |
| YDR154C | | 21268.57 | 56534.93 | ↑ | 2.65 |
| YGR236C | SPG1 | 17717.80 | 64439.96 | ↑ | 3.64 |
| YHR066C | RSC30 | 27020.16 | 65110.42 | ↑ | 2.41 |
| YGR182C | | 8171.02 | 34669.96 | ↑ | 4.24 |
| YDR544C | | 14797.70 | 37704.91 | ↑ | 2.55 |
| YHR162W | | 13836.79 | 33381.64 | ↑ | 2.41 |
| YGR243W | | 30829.66 | 59765.39 | ↑ | 1.94 |
| YHR050C | PEG2 | 14008.24 | 29603.16 | ↑ | 2.11 |
| YEL071W | DLD3 | 19467.41 | 35273.39 | ↑ | 1.81 |
| YDR133C | | 83074.54 | 62986.96 | ↓ | 1.32 |
| YDR134C | | 83111.03 | 16839.53 | ↓ | 4.94 |
| YHL021C | | 46028.06 | 8577.00 | ↓ | 5.37 |
| YKL054C | VID31 | 28018.46 | 66537.91 | ↑ | 2.37 |
| YLR311C | | 7803.52 | 31160.73 | ↑ | 3.89 |
| YHR107W | | 13453.15 | 78850.98 | ↑ | 5.86 |
| YKL066W | | 6751.84 | 24129.32 | ↑ | 2.76 |
| YHR173W-A | | 38338.83 | 60514.70 | ↑ | 1.58 |
| YML053C | | 23670.86 | 66254.48 | ↑ | 2.80 |
| YDR121C | | 17039.58 | 58016.58 | ↑ | 3.40 |
| YOL106W | | 19817.67 | 69853.66 | ↑ | 3.51 |
| YML338W | | 17864.90 | 49911.08 | ↑ | 2.79 |
| YJRI15W | | 84658.02 | 98161.71 | ↑ | 1.16 |
| Cellular role: Small molecule transport | | | | | |
| YOR267C | HFK1 | 90123.84 | 86824.51 | ↑ | 1.07 |

Table 4: Overview of the differentially expressed genes after 2h Bax expression
Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

| | | Cellular role: Protein modification/degradation | | | |
|-----------|-------|-------------------------------------------------|-----------|---|------|
| YCL052C | PBN1 | 5284.22 | 8115.70 | ↑ | 1.55 |
| YDL147W | RPN5 | 22368.40 | 47857.67 | ↑ | 2.14 |
| YOR261C | RPN6 | 27349.25 | 42198.05 | ↑ | 1.54 |
| YGR132C | PBH1 | 5252.03 | 8459.53 | ↑ | 1.61 |
| YBR139W | | 9458.26 | 3611.21 | ↑ | 2.62 |
| | | Cellular role: Unknown | | | |
| YDR202C | PAV2 | 7483.71 | 10089.19 | ↑ | 1.35 |
| YHR082C | | 4893.97 | 9894.82 | ↑ | 2.02 |
| YDR366C | | 25468.2 | 59682.92 | ↑ | 2.34 |
| YBL109W | | 24803.62 | 37444.64 | ↑ | 1.51 |
| YDR154C | | 21166.26 | 33434.35 | ↑ | 1.58 |
| YEL071W | DLD3 | 34153.85 | 44083.39 | ↑ | 1.29 |
| YGR236C | SPG1 | 16978.52 | 31419.12 | ↑ | 1.85 |
| YGR182C | | 30569.31 | 56805.05 | ↑ | 1.92 |
| YDR544C | | 15697.14 | 24421.99 | ↑ | 1.53 |
| YHR162W | | 28610.34 | 33794.73 | ↑ | 1.27 |
| YHR066C | RSC30 | 33372.66 | 68425.24 | ↑ | 2.05 |
| YDR133C | | 73520.99 | 82984.59 | ↑ | 1.20 |
| YDR134C | ADY2 | 17240.59 | 9776.23 | ↓ | 1.46 |
| YCH010C | | 72723.66 | 53767.35 | ↑ | 7.44 |
| YGR069W | | 65418.73 | 2198.04 | ↓ | 1.22 |
| YIL057C | | 16510.16 | 6509.91 | ↓ | 7.51 |
| YGL072C | | 12209.88 | 11525.24 | ↓ | 1.88 |
| YGL080W | | 22560.76 | 24680.47 | ↑ | 1.96 |
| YLR311C | | 11095.31 | 103422.48 | ↑ | 2.22 |
| YJRI15W | | 74767.79 | 11477.42 | ↑ | 1.38 |
| YMR099C | | 7057.15 | 48886.91 | ↑ | 1.63 |
| YMR173W-A | | 31901.05 | 34695.33 | ↑ | 1.47 |
| YML132W | COO3 | 24648.97 | 25433.87 | ↑ | 1.42 |
| YKL066W | | 13561.84 | 11920.21 | ↑ | 1.87 |
| YIL142C | | 7205.86 | 11569.83 | ↑ | 1.85 |
| YLR546C | | 8447.57 | 78636.82 | ↑ | 1.79 |
| YLR053C | | 41161.10 | 28661.23 | ↑ | 1.91 |
| YMR110C | | 19410.84 | 28948.72 | ↑ | 1.53 |
| YKR075C | | 19104.57 | 59452.09 | ↑ | 1.57 |
| YOR121C | | 38492.56 | | ↑ | 1.63 |

| | | Cellular role : Unknown | | | |
|---------------------------------------------|--------|-------------------------|----------|---|------|
| YOL106W | | 31382.10 | 78684.72 | ↑ | 2.44 |
| YNL339W | | 24117.93 | 39891.22 | ↑ | 1.62 |
| YNL194C | | 9817.33 | 14813.60 | ↑ | 1.52 |
| YKL065C | YET1 | 52422.65 | 33784.03 | ↓ | 1.55 |
| YMR009W | | 20868.22 | 9519.29 | ↓ | 2.17 |
| YLL144W | | 10316.92 | 3122.77 | ↓ | 3.30 |
| YNL128C | MSC1 | 584128.13 | 25434.11 | ↓ | 2.29 |
| YNL179C | | 21838.98 | 10883.88 | ↓ | 2.02 |
| YOL109W | ZE01 | 22711.98 | 6581.11 | ↓ | 3.45 |
| YNR002C | FUN34 | 18241.25 | 9752.25 | ↓ | 1.87 |
| Cellular role : Chromalins structure | | | | | |
| YDR224C | HTB1 | 25358.73 | 30827.54 | ↑ | 1.22 |
| YBL002W | HTB2 | 9241.68 | 14281.54 | ↑ | 1.54 |
| YBL003C | HT42 | 3453.55 | 6553.49 | ↑ | 1.90 |
| YNL031C | HTT2 | 13378.02 | 2348.84 | ↓ | 5.69 |
| Cellular role : Polymerase II transcription | | | | | |
| YBR269W | SNF5 | 59542.27 | 65885.13 | ↑ | 1.11 |
| YDR073W | SNF11 | 12190.01 | 23088.03 | ↑ | 1.89 |
| YMR043W | MCM1 | 68457.16 | 77022.05 | ↑ | 1.16 |
| YPL089C | RLM1 | 49844.99 | 60624.28 | ↑ | 1.22 |
| Cellular role : Signal transduction | | | | | |
| YDR099W | BMH2 | 55902.13 | 73874.51 | ↑ | 1.32 |
| Cellular role : Cell stress | | | | | |
| YBL084C | PRX1 | 11203.87 | 14815.42 | ↑ | 1.32 |
| YBR101C | | 25016.27 | 35781.64 | ↑ | 1.43 |
| YLR043C | TRX1 | 10864.53 | 3912.03 | ↓ | 2.78 |
| YGR209C | TRX2 | 30492.33 | 37829.20 | ↑ | 1.24 |
| YER103W | SSA4 | 8763.38 | 15789.18 | ↑ | 1.80 |
| YHR055C | CUP1B | 18824.43 | 77613.05 | ↑ | 4.12 |
| YHR053C | CUP1A | 32728.82 | 63538.72 | ↑ | 1.94 |
| YDR256C | CTA1 | 9814.29 | 4232.17 | ↓ | 2.27 |
| YCR021C | HSP30 | 8090.05 | 3604.78 | ↓ | 2.24 |
| YCL035C | GRX1 | 28437.57 | 12843.99 | ↓ | 2.21 |
| YGR086C | | 38708.12 | 24272.57 | ↓ | 1.52 |
| YFL014W | HSP12 | 61868.64 | 23288.19 | ↓ | 2.66 |
| YOR031W | CR55 | 6015.69 | 14519.12 | ↑ | 2.41 |
| YMR251W-A | HOR7 | 17731.14 | 4231.39 | ↓ | 4.19 |
| YOR120W | GCY1 | 114252.98 | 78052.05 | ↓ | 1.46 |
| Cellular role : Protein synthesis | | | | | |
| YAL003W | EFB1 | 3044.80 | 5772.68 | ↑ | 1.90 |
| YOL127W | RPL25 | 6268.96 | 12055.41 | ↑ | 1.92 |
| YHR010W | RPL27 | 4057.16 | 10856.34 | ↑ | 2.68 |
| YLR325C | RPL38 | 5401.85 | 12955.89 | ↑ | 2.40 |
| YLL189W | RPL39 | 2044.64 | 8010.67 | ↑ | 3.92 |
| YIL148W | RPL40A | 5052.35 | 11595.54 | ↑ | 2.30 |
| YKR094C | RPL40B | 3984.57 | 10011.13 | ↑ | 2.54 |
| YOL139C | CDC33 | 4132.18 | 8958.14 | ↑ | 2.17 |

| | | Cellular role : Protein folding | | | |
|------------------------------------------|---------|---------------------------------|-----------|---|------|
| YLR216C | CPR8 | 20353.43 | 32713.37 | ↑ | 1.61 |
| YKL177W | SBA1 | 11144.25 | 1500.58 | ↓ | 7.43 |
| Cellular role : Vesicular transport | | | | | |
| YCR009C | RVS161 | 5350.32 | 9780.92 | ↑ | 1.83 |
| YHR161C | YAP180A | 25138.83 | 32481.67 | ↑ | 1.28 |
| YBL078C | AUT7 | 16528.91 | 9843.25 | ↓ | 1.88 |
| Cellular role : Carbohydrate metabolism | | | | | |
| YBL058W | SHP1 | 4626.50 | 8178.94 | ↑ | 1.77 |
| YBR149W | ARA1 | 30708.41 | 9837.76 | ↓ | 3.19 |
| YDR178W | SDH4 | 14880.91 | 8237.35 | ↓ | 2.39 |
| YHR094C | HXT1 | 30389.99 | 18383.00 | ↓ | 1.65 |
| YMR011W | HXT2 | 39524.90 | 21221.86 | ↓ | 1.88 |
| YDR345C | HXT3 | 77025.40 | 56749.40 | ↓ | 1.38 |
| YDR343C | HXT6 | 73149.70 | 8678.17 | ↓ | 8.43 |
| YDR342C | HXT7 | 75331.76 | 27052.43 | ↓ | 2.78 |
| YKL060C | FBA1 | 16273.54 | 21323.23 | ↑ | 1.31 |
| Cellular role : Cell cycle control | | | | | |
| YBR133C | HSL7 | 32903 | 41884.32 | ↑ | 1.28 |
| Cellular role : Energy generation | | | | | |
| YMR256C | COX7 | 18558.01 | 40422.91 | ↑ | 2.18 |
| YML129C | COX14 | 11418.54 | 21798.88 | ↑ | 1.91 |
| YFR033C | QCR6 | 9159.48 | 13398.87 | ↑ | 1.48 |
| YDR29C | QCR7 | 24821.75 | 16556.87 | ↓ | 1.50 |
| YLL168W | QCR8 | 15554.30 | 24509.28 | ↑ | 1.58 |
| YHR001W-A | QCR10 | 12418.35 | 23465.31 | ↑ | 1.68 |
| YBR039W | ATP3 | 11709.78 | 3088.19 | ↓ | 3.78 |
| YPL078C | ATP4 | 11325.84 | 13769.72 | ↑ | 1.22 |
| YPL271W | ATP15 | 3281.75 | 7839.05 | ↑ | 2.40 |
| YLR327C | | 51742.90 | 128511.27 | ↑ | 2.48 |
| YLR294C | | 15832.81 | 38544.44 | ↑ | 2.43 |
| YAL060W | FUN49 | 11792.72 | 5778.91 | ↓ | 2.04 |
| Cellular role : Small molecule transport | | | | | |
| YDR276C | SNA1 | 19337.39 | 12392.29 | ↓ | 1.58 |
| YGR197C | SNG1 | 4766.18 | 10484.09 | ↑ | 2.20 |
| YHR039C-B | VMA10 | 21190.93 | 10592.88 | ↓ | 2.00 |
| YOR267C | HAK1 | 111849.17 | 101338.10 | ↓ | 1.10 |
| Cellular role : RNA processing | | | | | |
| YGR250C | | 8709.92 | 17358.43 | ↑ | 1.99 |
| Cellular role : Cell wall maintenance | | | | | |
| YER150W | SPH1 | 55592.73 | 22403.59 | ↓ | 2.48 |
| YLR110C | CCW12 | 35147.41 | 5786.88 | ↓ | 6.07 |
| Cellular role : Cell polarity | | | | | |
| YOR122C | PPY1 | 14459.45 | 20176.41 | ↑ | 1.40 |
| Cellular role : Amino acid metabolism | | | | | |
| YPR035W | GLN1 | 20894.14 | 7522.05 | ↓ | 2.78 |

Table 5: Overview of the differentially expressed genes after 3h Bax expression

Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

| Gene | Gene | Normalized intensities | Log2 fold change | P-value |
|----------------------------------------|--------|------------------------|------------------|---------|
| Cellular role: Cell cycle control | | | | |
| YBR133C | HSL7 | 63582.10 | 43191.28 | 1.47 |
| Cellular role: Cell polarity | | | | |
| YBL065W | BOI1 | 32734.79 | 23497.41 | 1.39 |
| Cellular role: Chromatine structure | | | | |
| YDR545W | YRF1-1 | 20111.51 | 11479.67 | 1.75 |
| Cellular role: Energy generation | | | | |
| YGR005C | CIT2 | 11882.42 | 25632.94 | 2.16 |
| YGR183C | OCR9 | 74474.20 | 11510.99 | 6.47 |
| YOL126C | MDH2 | 55984.88 | 17978.10 | 3.11 |
| Cellular role: Carbohydrate metabolism | | | | |
| YBR019C | GAL10 | 3092.50 | 15897.54 | 5.08 |
| YDR345C | HXT3 | 14088.41 | 25657.68 | 1.82 |
| YKR097W | POK1 | 50736.44 | 20858.02 | 2.43 |
| Cellular role: Signal transduction | | | | |
| YDR099W | BMH2 | 63285.16 | 56028.91 | 1.13 |
| Cellular role: Protein synthesis | | | | |
| YHR010W | RPL27A | 23254.90 | 7217.14 | 3.22 |
| YLR325C | RPL38 | 26725.96 | 9121.29 | 2.93 |
| Cellular role: Cell stress | | | | |
| YFL014W | HSP12 | 40848.44 | 69781.91 | 1.71 |
| YHR053C | CUP1A | 20399.10 | 65037.14 | 3.19 |
| YHR055C | CUP1B | 21783.09 | 64594.58 | 2.97 |
| YMR173W | DDR48 | 75407.18 | 36354.37 | 2.07 |
| YOL052C-A | DDR2 | 20479.72 | 33702.23 | 1.65 |
| Cellular role: Unknown | | | | |
| YIL057C | | 7802.78 | 24104.02 | 3.17 |
| YHR056C | RSC30 | 41473.41 | 64809.08 | 1.56 |
| YDR544C | | 55075.67 | 29731.72 | 1.85 |
| YKR040C | | 48049.71 | 59649.47 | 1.24 |
| YNL338W | | 86107.91 | 30045.62 | 2.87 |
| YLR115W | | 74889.58 | 81238.98 | 1.08 |
| YBL109W | | 64754.79 | 57185.99 | 1.13 |
| YMR173W-A | | 75407.16 | 36354.37 | 2.07 |

Table 6: Overview of the differentially expressed genes after 6h Bax expression

Comparison: INVSc1 YipUTL versus INVSc1 YipUTYLB

| Gene | Gene | Normalized intensities | Log2 fold change | P-value |
|------------------------------------|--------|------------------------|------------------|---------|
| Cellular role: Cell stress | | | | |
| YDR171W | HSP42 | 13484.04 | 27183.07 | 2.02 |
| YFL014W | HSP12 | 41197.12 | 28081.08 | 1.42 |
| YDR513W | THP1 | 18985.22 | 12935.62 | 1.54 |
| YCL055C | GRX1 | 31735.39 | 12930.71 | 2.45 |
| YGR209C | TRX2 | 54455.65 | 47569.21 | 1.14 |
| YHR053C | CUP1A | 81488.84 | 15289.39 | 5.33 |
| YHR055C | CUP1B | 81278.95 | 20031.69 | 4.06 |
| YMR251W-A | HOH7 | 18824.54 | 5914.28 | 3.18 |
| Cellular role: Signal transduction | | | | |
| YDR099W | BMH2 | 28412.89 | 58598.42 | 1.99 |
| Cellular role: Protein synthesis | | | | |
| YGL147C | RPL9A | 13655.68 | 1585.97 | 8.61 |
| YGR085C | RPL11B | 27465.15 | 3761.35 | 7.24 |
| YDR418W | RPL12B | 14417.77 | 1555.24 | 9.27 |
| YLR029C | RPL15A | 37122.11 | 9321.81 | 3.98 |
| YOR312C | RPL20B | 50334.94 | 5708.59 | 8.82 |
| YBR191W | RPL21A | 21740.90 | 2571.30 | 8.46 |
| YPL079W | RPL21B | 31059.43 | 5023.61 | 6.18 |
| YOL127W | RPL25 | 75971.72 | 11749.17 | 6.47 |
| YHR010W | RPL27A | 45716.64 | 8098.40 | 5.85 |
| YDR471W | RPL27B | 14638.79 | 2613.40 | 5.60 |
| YDL075W | RPL31A | 11969.47 | 2611.53 | 4.58 |
| YBL092W | RPL32 | 7872.80 | 857.85 | 9.18 |
| YDL191W | RPL35A | 28582.59 | 6046.25 | 4.73 |
| YDL136W | RPL35B | 25433.48 | 5084.51 | 5.02 |
| YLR325C | RPL38 | 48051.23 | 8217.18 | 5.85 |
| YLR148W | RPL40A | 47028.85 | 9543.85 | 4.93 |
| YKR094C | RPL40B | 39900.50 | 5957.78 | 6.70 |
| YHR141C | RPL42B | 10163.88 | 937.21 | 10.84 |
| YML063W | RPS1B | 15916.48 | 1144.54 | 13.91 |
| YGL123W | RPS2 | 12505.58 | 2243.26 | 5.57 |
| YOR096W | RPS7A | 24184.37 | 3223.60 | 7.50 |
| YBL072C | RPS8A | 17188.50 | 3233.30 | 5.32 |
| YER102W | RPS8B | 16234.83 | 1791.18 | 9.06 |
| YDR169W | RPS9B | 10075.22 | 2160.89 | 4.88 |
| YOR293W | RPS10A | 51787.23 | 12110.74 | 4.28 |
| YDR064W | RPS13 | 9736.57 | 1587.67 | 6.13 |
| YDR450W | RPS18A | 37813.71 | 5874.80 | 6.86 |
| YML026C | RPS19B | 14458.01 | 2027.28 | 7.13 |
| YKL156W | RPS27A | 23725.18 | 11117.26 | 2.13 |
| YLR167W | RPS31 | 38648.54 | 2611.97 | 14.80 |
| YIL138C | TIF2 | 20154.61 | 7264.86 | 2.77 |
| Cellular role: Energy metabolism | | | | |
| YGR183C | OCR9 | 57357.59 | 80447.53 | 1.40 |
| YDL004W | ATP16 | 25047.95 | 10988.85 | 2.28 |
| YKL150W | MCRI | 50931.46 | 37076.83 | 1.37 |

| | | | | | |
|--------------------------------------------|-------|----------|----------|---|------|
| YLR038C | COX12 | 39508.08 | 29534.70 | ↓ | 1.34 |
| Cellular role: Unknown | | | | | |
| YDR442W | | 14854.81 | 2242.42 | ↓ | 6.54 |
| YDR134C | | 17025.59 | 10561.72 | ↓ | 1.61 |
| YHR056C | RSC30 | 81350.52 | 31447.10 | ↓ | 2.59 |
| YKR040C | | 48390.21 | 90125.88 | ↑ | 1.86 |
| YLR414C | | 13463.40 | 8085.92 | ↓ | 1.67 |
| YLR312C | | 25589.67 | 16184.57 | ↓ | 1.58 |
| YJL188C | BUD19 | 22074.09 | 4526.39 | ↓ | 4.88 |
| YOR265W | | 75099.98 | 61898.00 | ↓ | 1.21 |
| YOL109W | ZEO1 | 68287.15 | 35502.43 | ↓ | 1.87 |
| Cellular role: Chromatine structure | | | | | |
| YBR009C | HHF1 | 11173.15 | 5416.74 | ↓ | 2.08 |
| YNL030W | HHF2 | 31368.74 | 20132.23 | ↓ | 1.56 |
| Cellular role: Nucleotide metabolism | | | | | |
| YDR399W | HPT1 | 13339.03 | 5333.81 | ↓ | 2.50 |
| Cellular role: Polymerase II transcription | | | | | |
| YEL009C | GCN4 | 34617.88 | 20798.63 | ↓ | 1.66 |
| YPL037C | EGD1 | 17882.37 | 8228.01 | ↓ | 2.17 |
| Cellular role: Vesicular transport | | | | | |
| YBL078C | AUT7 | 42661.70 | 32333.01 | ↓ | 1.32 |
| YOR327C | SNC2 | 22718.56 | 13704.48 | ↓ | 1.66 |
| Cellular role: Small molecule transport | | | | | |
| YHR039C-B | VMA10 | 44429.30 | 23826.51 | ↓ | 1.86 |
| Cellular role: Cell wall maintenance | | | | | |
| YKL097W-A | CWP2 | 13529.83 | 1617.20 | ↓ | 8.37 |
| Cellular role: Carbohydrate metabolism | | | | | |
| YKL060C | FBA1 | 33329.74 | 10367.82 | ↓ | 3.21 |

Table 7:

| Sequence ID NO | ORF | GENE | 30 min | 1h | 2h | 3h | 6h |
|----------------|-----------|--------|--------|-------|-------|-------|-------|
| SEQ ID NO 17 | YAL003W | EFB1 | | | 1.90 | | |
| SEQ ID NO 19 | YAL060W | FUN49 | | | -2.00 | | |
| SEQ ID NO 21 | YBL002W | HTB2 | -4.69 | | 1.54 | | |
| SEQ ID NO 23 | YBL058W | SHI1 | | | 1.77 | | |
| SEQ ID NO 25 | YBL064C | PRX1 | 1.90 | | 1.32 | | -5.32 |
| SEQ ID NO 27 | YBL072C | RPS8A | | | | | |
| SEQ ID NO 29 | YBL081W | | 1.01 | 1.88 | | | |
| SEQ ID NO 31 | YBL085W | BOI1 | 2.42 | 1.52 | | -1.39 | -8.18 |
| SEQ ID NO 33 | YBL092W | RPL32 | | | 2.76 | | |
| SEQ ID NO 35 | YBL109W | | 1.89 | 2.76 | 1.51 | -1.13 | -2.08 |
| SEQ ID NO 37 | YBR009C | HMF1 | -3.89 | | | | |
| SEQ ID NO 39 | YBR019C | GAL10 | | | -3.70 | 5.08 | |
| SEQ ID NO 41 | YBR039W | ATP3 | | 2.11 | | | |
| SEQ ID NO 43 | YBR050C | REG2 | 3.07 | | 2.02 | | |
| SEQ ID NO 45 | YBR062C | | | | | | |
| SEQ ID NO 47 | YBR089C-A | NHP88 | -3.60 | | 1.43 | | |
| SEQ ID NO 49 | YBR101C | | | | | | |
| SEQ ID NO 51 | YBR112C | SSN6 | 2.45 | 1.28 | | -1.47 | -4.88 |
| SEQ ID NO 53 | YBR133C | HSL7 | 2.00 | 2.84 | 1.28 | | -8.46 |
| SEQ ID NO 55 | YBR139W | | | | -2.60 | | |
| SEQ ID NO 57 | YBR149W | APA1 | -3.70 | | -3.11 | | |
| SEQ ID NO 59 | YBR169W | RPS8B | | | | | |
| SEQ ID NO 61 | YBR191W | RPL21A | | | | | |
| SEQ ID NO 63 | YBR289W | SNF5 | 2.18 | | 1.11 | | |
| SEQ ID NO 65 | YCL035C | GRX1 | -8.40 | | -2.20 | | -2.45 |
| SEQ ID NO 67 | YCL052C | PBN1 | | | 1.55 | | |
| SEQ ID NO 69 | YCR004C | YCP4 | 4.09 | | | 2.16 | |
| SEQ ID NO 71 | YCR005C | CIT2 | | | 1.83 | | |
| SEQ ID NO 73 | YCR009C | RVS181 | | | -1.40 | | |
| SEQ ID NO 75 | YCR010C | | | | | | |
| SEQ ID NO 77 | YCR013C | | 3.80 | | | | |
| SEQ ID NO 79 | YCR021C | HSP30 | | | -2.20 | | -2.28 |
| SEQ ID NO 81 | YDL004W | ATP16 | -12.16 | | | | |
| SEQ ID NO 83 | YDL059C | RAO59 | 6.72 | | | | -4.58 |
| SEQ ID NO 85 | YDL075W | RPL31A | | | 2.14 | | -6.13 |
| SEQ ID NO 87 | YDL147W | RPN5 | 1.66 | | | | |
| SEQ ID NO 89 | YDR064W | RPS13 | | | | | |
| SEQ ID NO 91 | YDR073W | SNF11 | | | 1.89 | | |
| SEQ ID NO 93 | YDR099W | BMH2 | 1.86 | 1.29 | 1.32 | -1.13 | 1.99 |
| SEQ ID NO 95 | YDR133C | | | -1.32 | -1.20 | | |
| SEQ ID NO 97 | YDR134C | | | -4.94 | -7.40 | | -1.61 |
| SEQ ID NO 99 | YDR145W | TAF61 | 1.89 | 2.77 | | | |
| SEQ ID NO 101 | YDR154C | | 3.55 | 2.85 | 1.56 | | 2.02 |
| SEQ ID NO 103 | YDR171W | HSP42 | | | | | |
| SEQ ID NO 105 | YDR178W | SDH4 | | | -2.30 | | |
| SEQ ID NO 107 | YDR202C | RAV2 | | | 1.35 | | |
| SEQ ID NO 109 | YDR216W | ADR1 | -3.42 | 3.11 | | | |
| SEQ ID NO 111 | YDR224C | HTB1 | -2.91 | 4.07 | 1.22 | | |
| SEQ ID NO 113 | YDR253C | MET32 | 2.58 | | | | |
| SEQ ID NO 115 | YDR256C | CTA1 | | | -2.20 | | |
| SEQ ID NO 117 | YDR276C | SNA1 | -13.38 | | -1.50 | | |

| Sequence ID NO | ORF | GENE | 30 min | 1h | 2h | 3h | 6h |
|----------------|-----------|---------|--------|-------|-------|-------|-------|
| SEQ ID NO 118 | YDR342C | HXT7 | -2.76 | -2.94 | -2.70 | | |
| SEQ ID NO 121 | YDR343C | HXT6 | -2.40 | -1.17 | -8.40 | | |
| SEQ ID NO 123 | YDR345C | HXT3 | -22.45 | -1.89 | -1.30 | 1.82 | |
| SEQ ID NO 125 | YDR366C | | 1.44 | 3.18 | 2.34 | | |
| SEQ ID NO 127 | YDR377W | ATP17 | -18.05 | | | | -2.50 |
| SEQ ID NO 129 | YDR399W | HP17 | | | | | -9.27 |
| SEQ ID NO 131 | YDR418W | RPL128 | | | | | -1.54 |
| SEQ ID NO 133 | YDR513W | TR1 | -1.68 | | 1.53 | -1.85 | |
| SEQ ID NO 135 | YDR544C | | 1.99 | 2.55 | | -1.75 | -1.68 |
| SEQ ID NO 137 | YDR545W | YRF1.1 | | | | | |
| SEQ ID NO 139 | YEL009C | GCN4 | -5.46 | | | | |
| SEQ ID NO 141 | YEL022W | MCN3 | 1.89 | | | | |
| SEQ ID NO 143 | YEL039C | CYC7 | -5.06 | | | | |
| SEQ ID NO 145 | YEL071W | DLD3 | 3.09 | 1.81 | 1.29 | | |
| SEQ ID NO 147 | YER103W | SSA4 | | | 1.80 | | |
| SEQ ID NO 149 | YER112W | US51 | 2.46 | | -2.40 | | |
| SEQ ID NO 151 | YER150W | SP1 | 1.98 | 1.95 | | | |
| SEQ ID NO 153 | YFR010W | UBP6 | -2.28 | | 1.46 | | |
| SEQ ID NO 155 | YFR033C | OCN6 | | | | | |
| SEQ ID NO 157 | YFR052W | RPV12 | 2.68 | | -1.80 | | -5.57 |
| SEQ ID NO 159 | YGL072C | | -6.20 | | -1.80 | | |
| SEQ ID NO 161 | YGL080W | | -7.28 | | | | |
| SEQ ID NO 163 | YGL123W | RP52 | -5.83 | | | | |
| SEQ ID NO 165 | YGR008C | STR2 | 2.87 | | | | |
| SEQ ID NO 167 | YGR023W | MTL1 | 1.04 | | | | |
| SEQ ID NO 169 | YGR034W | RPL26B | 1.67 | | -1.20 | | |
| SEQ ID NO 171 | YGR069W | ROM1 | 2.34 | | -1.50 | | |
| SEQ ID NO 173 | YGR070W | | | | -1.81 | | |
| SEQ ID NO 175 | YGR086C | PHB1 | -2.76 | | | | |
| SEQ ID NO 177 | YGR132C | PRE9 | -7.24 | | | | |
| SEQ ID NO 179 | YGR135W | CYS4 | 4.61 | | | | |
| SEQ ID NO 181 | YGR155W | TDH3 | | -2.72 | 2.20 | | |
| SEQ ID NO 183 | YGR192C | SNG1 | | | 1.24 | | -1.14 |
| SEQ ID NO 185 | YGR197C | TRX2 | | | 1.99 | | |
| SEQ ID NO 187 | YGR209C | | | 1.94 | | | |
| SEQ ID NO 189 | YGR243W | | | | 1.89 | | |
| SEQ ID NO 191 | YGR250C | | | -5.37 | | | |
| SEQ ID NO 193 | YHL021C | | | | 1.89 | | |
| SEQ ID NO 195 | YHR001W-A | OCR10 | -7.08 | | -2.00 | | -1.86 |
| SEQ ID NO 197 | YHR039C-B | VMA10 | -1.88 | 1.95 | 1.94 | 3.19 | -5.33 |
| SEQ ID NO 199 | YHR053C | CUP1A | -2.77 | 2.33 | 4.12 | 2.97 | -4.06 |
| SEQ ID NO 201 | YHR055C | CUP1B | -1.25 | 2.41 | 2.05 | 1.56 | -2.59 |
| SEQ ID NO 203 | YHR056C | | -15.94 | | -1.60 | | |
| SEQ ID NO 205 | YHR094C | HXT1 | 2.42 | | | | |
| SEQ ID NO 207 | YHR095W | | -5.37 | | | | |
| SEQ ID NO 209 | YHR138C | YAP180A | 2.30 | 2.99 | 1.29 | | |
| SEQ ID NO 211 | YHR161C | | | 2.41 | 1.27 | | |
| SEQ ID NO 213 | YHR162W | | | | | | |
| SEQ ID NO 215 | YHR179W | OYE2 | 17.58 | | -7.50 | 3.17 | |
| SEQ ID NO 217 | YIL057C | SER33 | -31.34 | | | | |
| SEQ ID NO 219 | YIL074C | | 4.20 | | | | |
| SEQ ID NO 221 | YIR037W | GPX3 | 2.77 | | | | |

| Sequence ID NO | ORF | GENE | 30 min | 1h | 2h | 3h | 6h |
|----------------|-----------|--------|--------|-------|-------|-------|-------|
| SEQ ID NO 223 | YIL138C | TRF2 | | | 1.65 | | -2.77 |
| SEQ ID NO 225 | YIL142C | | | | -3.30 | | |
| SEQ ID NO 227 | YIL144W | | -6.29 | | 1.58 | | |
| SEQ ID NO 229 | YIL161W | | | | | | |
| SEQ ID NO 231 | YIL166W | OCR8 | -2.04 | 1.16 | 1.38 | -1.08 | |
| SEQ ID NO 233 | YJR096W | | 1.58 | 2.37 | 1.31 | | -3.21 |
| SEQ ID NO 235 | YJR115W | VID31 | 2.13 | | -1.55 | | |
| SEQ ID NO 237 | YKL054C | FBA1 | | | | | |
| SEQ ID NO 239 | YKL080C | YET1 | -5.43 | 2.76 | 1.87 | | |
| SEQ ID NO 241 | YKL085C | | | | | | |
| SEQ ID NO 243 | YKL086W | | | | | | |
| SEQ ID NO 245 | YKL097W-A | CWP2 | | | -7.43 | | -8.37 |
| SEQ ID NO 247 | YKL117W | SB1 | -3.43 | 1.39 | | -1.37 | |
| SEQ ID NO 249 | YKL150W | MCN1 | | | | -2.13 | |
| SEQ ID NO 251 | YKL156W | RP527A | -6.55 | | | | |
| SEQ ID NO 253 | YKL196C | YKT6 | 1.98 | | | 1.86 | |
| SEQ ID NO 255 | YKR040C | | | | 1.57 | | |
| SEQ ID NO 257 | YKR075C | | | | | | |
| SEQ ID NO 259 | YKR076W | ECM4 | 4.88 | 1.67 | | -2.43 | |
| SEQ ID NO 261 | YKR092C | SRP40 | 2.70 | | | | -3.98 |
| SEQ ID NO 263 | YKR097W | PCK1 | | | | | -1.34 |
| SEQ ID NO 265 | YLR029C | RPL15A | -9.68 | | -2.78 | | |
| SEQ ID NO 267 | YLR038C | COX12 | -13.13 | | 1.91 | | |
| SEQ ID NO 269 | YLR043C | TRX1 | 2.50 | | | | |
| SEQ ID NO 271 | YLR053C | | | -6.83 | -6.07 | | |
| SEQ ID NO 273 | YLR109W | AHP1 | | 2.40 | 1.61 | | |
| SEQ ID NO 275 | YLR110C | ENT2 | 3.24 | 5.74 | 2.43 | | |
| SEQ ID NO 277 | YLR206W | CPH6 | 3.02 | 3.99 | 2.22 | | |
| SEQ ID NO 279 | YLR216C | | | | | | |
| SEQ ID NO 281 | YLR294C | | | | | | |
| SEQ ID NO 283 | YLR311C | | -2.10 | 1.04 | 2.48 | -1.58 | |
| SEQ ID NO 285 | YLR327C | | | | 1.79 | | |
| SEQ ID NO 287 | YLR346C | ECM19 | 2.77 | | | | -1.67 |
| SEQ ID NO 289 | YLR390W | | | | | | |
| SEQ ID NO 291 | YLR414C | | | 2.80 | | | |
| SEQ ID NO 293 | YML053C | | | | 1.91 | | |
| SEQ ID NO 295 | YML129C | COX14 | | | -2.17 | | |
| SEQ ID NO 297 | YML129W | COX3 | | | -1.86 | | |
| SEQ ID NO 299 | YMR011W | HXT2 | 2.15 | 2.56 | 1.16 | | |
| SEQ ID NO 301 | YMR019W | MCN1 | | | 1.63 | | |
| SEQ ID NO 303 | YMR043W | | -6.48 | 5.88 | 1.53 | | |
| SEQ ID NO 305 | YMR099C | | | | | | |
| SEQ ID NO 307 | YMR107W | | -3.32 | 1.58 | 1.47 | -2.07 | |
| SEQ ID NO 309 | YMR110C | | -64.41 | | | | |
| SEQ ID NO 311 | YMR173W | | -64.41 | | | | |
| SEQ ID NO 313 | YMR173W-A | DDR48 | -1.78 | 1.58 | | | |
| SEQ ID NO 315 | YMR251W | | -64.41 | | -4.19 | | -3.18 |
| SEQ ID NO 317 | YMR251W-A | | | 3.79 | 2.18 | | |
| SEQ ID NO 319 | YMR256C | COX7 | 2.42 | | | | |
| SEQ ID NO 321 | YMR273C | ZDS1 | -3.97 | | | | |
| SEQ ID NO 323 | YNL030W | HHF2 | | | | | |
| SEQ ID NO 325 | YNL031C | HHF2 | | | -5.89 | | -1.58 |

| Sequence ID NO | ORF | GENE | 30 min | 1h | 2h | 3h | 8h |
|----------------|-----------|--------|--------|--------|-------|-------|-------|
| SEQ ID NO 327 | YNL112W | DRP2 | 2.82 | | | | |
| SEQ ID NO 328 | YNL131W | TOM22 | -9.70 | | 1.52 | | |
| SEQ ID NO 331 | YNL134C | | 1.12 | | -2.02 | | |
| SEQ ID NO 333 | YNL143C | | 2.88 | | 1.62 | | |
| SEQ ID NO 335 | YNL179C | | 1.78 | 2.79 | -1.87 | -2.87 | |
| SEQ ID NO 337 | YNL338W | | | | | | |
| SEQ ID NO 339 | YNR002C | FUN34 | | | | | |
| SEQ ID NO 708 | YOL052C-A | DDR2 | | | | 1.65 | -1.87 |
| SEQ ID NO 341 | YOL106W | | | 3.51 | 2.44 | | |
| SEQ ID NO 343 | YOL109W | ZE01 | | | -3.45 | | |
| SEQ ID NO 345 | YOL126C | MDH2 | | 1.91 | 2.17 | -3.11 | |
| SEQ ID NO 347 | YOL139C | CDC33 | | | | | |
| SEQ ID NO 349 | YOL150C | | 17.69 | | | | |
| SEQ ID NO 351 | YOL151W | GRE2 | 9.20 | | | | |
| SEQ ID NO 353 | YOR120W | GCY1 | 1.54 | 3.40 | -1.48 | | |
| SEQ ID NO 355 | YOR121C | PFY1 | 2.81 | | 1.40 | | |
| SEQ ID NO 359 | YOR131C | | | 2.59 | 1.54 | | |
| SEQ ID NO 361 | YOR267C | APN8 | 1.76 | 1.07 | -1.10 | | |
| SEQ ID NO 363 | YOR287C | | -2.15 | | | | -1.21 |
| SEQ ID NO 365 | YOR285W | | -18.36 | | | | |
| SEQ ID NO 367 | YOR286W | | | | | | -1.86 |
| SEQ ID NO 369 | YOR327C | SNC2 | 2.19 | 1.92 | | | |
| SEQ ID NO 371 | YOR372C | ND01 | | -12.93 | | | |
| SEQ ID NO 373 | YOR374W | ALD4 | 4.02 | | | | |
| SEQ ID NO 375 | YOR382W | | | | | | -2.17 |
| SEQ ID NO 377 | YPL037C | EGD1 | -5.83 | | | | |
| SEQ ID NO 379 | YPL078C | ATP4 | -4.50 | | 1.22 | | |
| SEQ ID NO 381 | YPL079W | RPL21B | | | | | -6.18 |
| SEQ ID NO 383 | YPL085W | SEC16 | 2.28 | 2.74 | 1.22 | | |
| SEQ ID NO 385 | YPL089C | ALM1 | 1.94 | | | | |
| SEQ ID NO 387 | YPL180C | NAB3 | 2.80 | | | | |
| SEQ ID NO 389 | YPL201C | | -3.57 | | | | |
| SEQ ID NO 391 | YPR028W | ATP15 | -12.41 | | 2.40 | | |
| SEQ ID NO 393 | YPR035W | YIP2 | | | | | |
| SEQ ID NO 395 | | GLN1 | | | -2.78 | | |

| C. albicans 522 CDS's | | | | S. cerevisiae 11645 CDS's | | | |
|-----------------------|----------------------------------------|-----------------------------------------|------------------------------------------|----------------------------------|----------------------------|---------------------------------------|----------------------------------------------------|
| aa | codons | frequency; per thousand | total number | codon chosen for synthCabaX gene | wt mubaX gene | codons used in | frequency; per thousand |
| | | | | | | | |
| Ala | GCU GCC GCA GCG | 30.7 12.7 15.4 2 | 8686 4357 578 | x | 6 4 2 1 | 21.1 12.6 16.2 6.1 | 118595 70785 91018 34546 |
| Arg | CGU CGC CGA CGG AGA AGG | 5.9 0.7 3.5 0.8 23.6 2.7 | 1682 204 989 220 6673 769 | x | 1 1 3 3 1 2 | 6.5 2.6 3 1.7 21.3 9.3 | 36518 14571 16957 9801 119672 52057 |
| Asn | AAC AAU | 37.9 18.7 | 10731 5293 | x | 1 2 | 36 24.9 | 202351 140194 |
| Asp | GAU GAC | 43.6 14.7 | 12323 4152 | x | 5 7 | 37.8 20.4 | 212658 114451 |
| Cys | UGU UGC | 9.7 1.7 | 2757 493 | x | 1 1 | 8 4.7 | 44797 26357 |
| Gln | CAA CAG | 35.2 6.9 | 9964 1948 | x | 1 8 | 27.5 12.2 | 154529 68463 |
| Glu | GAA GAG | 49.5 11.5 | 14001 3252 | x | 3 10 | 45.9 19.1 | 257930 107568 |

TABLE 8 - continued

| C. albicans 522 CDS's | | | | | S. cerevisiae 11645 CDS's | | |
|-----------------------|--------|-------------------------|--------------|----------------------------------|------------------------------|-------------------------|--------------|
| aa | codons | frequency: per thousand | total number | codon chosen for synthCaBAX gene | codons used in wt muBAX gene | frequency: per thousand | total number |
| Gly | GGU | 33.5 | 9492 | x | 2 | 23.9 | 134515 |
| | GGC | 4.5 | 1281 | | 7 | 9.7 | 54629 |
| | GGA | 13.7 | 3874 | | 2 | 10.9 | 61481 |
| His | GGG | 7.7 | 2182 | | 8 | 6 | 33627 |
| | CAU | 14 | 3964 | | | 13.7 | 77260 |
| | CAC | 5.8 | 1642 | | | 7.8 | 43878 |
| Ile | AUU | 39.9 | 11281 | x | 3 | 30.2 | 169795 |
| | AUC | 14.2 | 4005 | | 7 | 17.1 | 96126 |
| | AUA | 12.3 | 3478 | | | 17.8 | 100027 |
| Leu | UUA | 1 | 295 | x | 2 | 26.3 | 148133 |
| | UUG | 36.1 | 10204 | | | 27.1 | 152590 |
| | CUU | 9.8 | 2777 | | | 12.2 | 68479 |
| | CUC | 2.5 | 694 | | | 5.4 | 30218 |
| | CUA | 4 | 1133 | | | 13.4 | 75414 |
| Lys | AAA | 48.6 | 13760 | x | 2 | 42.1 | 236746 |
| | AAG | 19.4 | 5477 | | 6 | 30.8 | 173174 |
| Met | AUG | 18.4 | 5219 | x | 8 | 20.9 | 117410 |
| Phe | UUU | 28.6 | 8100 | x | 4 | 26 | 146355 |
| | UUC | 15.9 | 4486 | | 7 | 18.2 | 102389 |

TABLE 8 - continued

| C. albicans 522 CDS's | | | | | S. cerevisiae 11645 CDS's | | |
|-----------------------|--------|-------------------------|--------------|----------------------------------|------------------------------|-------------------------|--------------|
| aa | codons | frequency: per thousand | total number | codon chosen for synthCaBAX gene | codons used in wt muBAX gene | frequency: per thousand | total number |
| Pro | CCU | 13.2 | 3722 | x | 1 | 13.6 | 76366 |
| | CCC | 3.6 | 1027 | | 5 | 6.8 | 38247 |
| | CCA | 26.6 | 7531 | | 1 | 18.2 | 102277 |
| | CCG | 2.4 | 686 | | | 5.3 | 29758 |
| Ser | CUG | 3.1 | 875 | x | 9 | 10.4 | 58583 |
| | UCU | 23.3 | 6595 | | 1 | 23.6 | 132608 |
| | UCC | 10.3 | 2928 | | 4 | 14.2 | 79928 |
| | UCA | 24.6 | 6955 | | 1 | 18.8 | 105570 |
| | UCG | 6.5 | 1836 | | | 8.6 | 48186 |
| | AGU | 23.6 | 6673 | | 5 | 14.2 | 79649 |
| | AGC | 4.5 | 1269 | | | 9.7 | 54330 |
| Thr | ACU | 30.7 | 8689 | x | 1 | 20.2 | 113634 |
| | ACC | 13.9 | 3928 | | 8 | 12.6 | 70777 |
| | ACA | 17.4 | 4928 | | 5 | 17.7 | 99759 |
| | ACG | 3.6 | 1019 | | 1 | 8 | 44817 |
| Trp | UGG | 11 | 3115 | x | 6 | 10.3 | 58092 |
| Tyr | UAU | 24 | 6782 | x | 2 | 18.8 | 105489 |
| | UAC | 11.6 | 3280 | | | 14.7 | 82483 |
| Val | GUU | 33.2 | 9391 | x | 1 | 22 | 123726 |
| | GUC | 10.3 | 2927 | | 3 | 11.6 | 65203 |
| | GUA | 8 | 2265 | | 7 | 11.8 | 66100 |
| | GUG | 10 | 2842 | | | 10.7 | 60033 |

TABLE 9: Regulation of 23 selected "Bax-specific" functions

| Cellular role: Amino-acid metabolism | | | | |
|-----------------------------------------------|---------|----------|----------|----------|
| ORF | Gene | Control | Bax | H2O2 |
| YOR302W | YOR302W | 11541.92 | 26808.35 | 8895.74 |
| Cellular role: Cell stress | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YML028W | YSA1 | 12889.91 | 2166.45 | 11327.36 |
| Cellular role: Chromatin/chromosome structure | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YBR009C | HHF1 | 2149.69 | 8655.43 | 2909.14 |
| YDR224C | HTB1 | 13661.40 | 55858.34 | 18829.27 |
| YNL030W | HHF2 | 8676.99 | 19603.93 | 4732.39 |
| Cellular role: Energy generation | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YBL059W | ATP1 | 2728.21 | 8786.71 | 1644.48 |
| YGR183C | OCR9 | 23181.54 | 81865.40 | 24053.00 |
| YJL166W | OCR8 | 5296.71 | 18093.93 | 5001.65 |
| YLR038C | COX12 | 7338.65 | 19935.69 | 5118.43 |
| Cellular role: Signal transduction | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YHR135C | YCK1 | 3939.64 | 8358.11 | 3707.17 |
| YOL100W | PKH2 | 2218.45 | 6088.96 | 2619.31 |
| Cellular role: Transcription factor | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YDR216W | ADR1 | 5925.91 | 18459.00 | 6434.43 |
| Cellular role: Unknown | | | | |
| ORF | Gene | Control | Bax | H2O2 |
| YDR504C | YDR504C | 2741.47 | 6908.49 | 2839.62 |
| YGR146C | YGR146C | 2099.74 | 5616.94 | 1303.89 |
| YGR236C | SPG1 | 17717.80 | 64439.96 | 24134.29 |
| YHR138C | YHR138C | 6218.30 | 14817.41 | 5220.50 |
| YJL142C | YJL142C | 6988.27 | 16006.02 | 8740.46 |
| YKL123W | YKL123W | 2826.82 | 5952.34 | 2766.04 |
| YLR414C | YLR414C | 4510.80 | 11867.69 | 3531.27 |
| YMR107W | YMR107W | 13453.15 | 78650.98 | 17417.00 |
| YOL099C | YOL099C | 3690.45 | 11604.72 | 5454.15 |
| YPL201C | YPL201C | 15960.14 | 33633.74 | 7449.66 |
| YJL060W | YJL060W | 8798.50 | 2406.39 | 6356.11 |

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CLAIMS

1. An isolated nucleic acid representing a synthetic BAX-gene selected from the group consisting of:
 - a) a nucleic acid comprising a sequence as represented by SEQ ID NO 1,
 - b) a nucleic acid comprising a fragment of a sequence of SEQ ID NO 1 and encoding a functional fragment of the sequence represented by SEQ ID NO 2,
 - c) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 3 to 10,
 - d) a nucleic acid which is more than 75 % identical to the nucleic acid as represented by SEQ ID NO 1, or to a nucleic acid according to the nucleic acid as defined in b) or c), and,
 - e) a nucleic acid as defined in any one of (a) to (i) interrupted by intervening DNA sequences,or a nucleic acid representing the complement of any of said nucleic acids as defined in (a) to (d).
2. An isolated nucleic acid according to claim 1 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.
3. A vector comprising a nucleic acid as defined in claim 1 or 2.
4. A vector according to claim 3 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
5. An expression vector according to claim 4 which comprises an inducible promoter
6. An expression vector according to claim 4 or 5 which comprises a sequence encoding a reporter molecule.
7. A vector according to any of claims 3 to 6 for inducing programmed cell death in *Candida* spp.
8. A host cell transformed, transfected or infected with a vector according to any of claims 3 to 7.
9. A host cell of claim 8 which is a bacterial, yeast or fungal cell.
10. A host cell according to claim 8 or 9 wherein said cell is a *Candida* spp. cell.
11. A genetically modified yeast or fungal cell according to claim 9 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.

12. A genetically modified *Candida* spp. cell according to claim 10 wherein said modification results in the onset of at least one pathway eventually leading to programmed cell death.
13. A method for identifying Bax-resistant yeast or fungi comprising the steps of:
 - a) providing (a) genetically modified yeast or fungi according to claim 11,
 - b) treating said genetically modified yeast or fungi with a mutagen,
 - c) isolating resistant yeast or fungal cells, and,
 - d) optionally identifying and/or characterizing mutated genes in said resistant yeast or fungal cells.
14. A method for identifying *Candida* spp. sequences which are differentially expressed in a pathway eventually leading to programmed cell death using a nucleic acid as defined in claim 1 or 2, a vector according to any of claims 3 to 7 or a genetically modified host cell according to claim 10.
15. A method for obtaining and identifying *Candida* spp. sequences involved in a pathway eventually leading to programmed cell death comprising the steps of:
 - a) providing a two hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 1 or a vector according to any of claims 3 to 7 as a bait and a *Candida* spp. cDNA library as a prey are expressed,
 - b) detecting an interaction between said polypeptide and a *Candida* spp. polypeptide encoded by said cDNA library, and,
 - c) identifying said *Candida* spp. polypeptide or cDNA.
16. A method for identifying inhibitors (or inhibitor sequences) of Bax-induced cell death comprising the steps of:
 - a) providing a genetically modified organism according to claim 10,
 - b) expressing a cDNA library in said genetically modified organism, and,
 - c) identifying a polypeptide or a cDNA which expression has a beneficial effect on the survival and/or growth of said genetically modified organism.
17. A method according to claim 16 wherein said genetically modified organism is a *Candida* spp.
18. An isolated *Candida* spp. nucleic acid identifiable by any of the methods of any of claims 12 to 17.
19. An isolated *Candida* spp. nucleic acid according to claim 18 selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % similar to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,

c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70 % identical to any of the amino acid sequences represented in SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732.

d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731,

e) a nucleic acid which is more than 70 % identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 433, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 717, 719, 721, 723, 725, 727, 729 and 731, and

f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in any of a) to d),

20. An isolated nucleic acid as defined in according to claim 19 which is DNA, cDNA, genomic DNA, synthetic DNA, or RNA wherein T is replaced by U.

21. An isolated nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 20 or the complement thereof.

22. An antisense molecule comprising a nucleic acid capable of selectively hybridizing to a nucleic acid as defined in any of claims 18 to 21.

23. A nucleic acid probe which selectively hybridises with any of the nucleic acid molecules as defined in claim 18 or 19.

24. A nucleic acid primer which selectively amplifies any of the nucleic acid molecules defined in claim 18 or 19.

25. An expression vector comprising a nucleic acid according to any of claims 18 to 22.
26. An expression vector according to claim 25 which is an expression vector wherein said nucleic acid is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.
27. An expression vector according to claim 25 or 26 which comprises an inducible promoter.
28. An expression vector according to any of claims 25 to 27 which comprises a sequence encoding a reporter molecule.
29. A host cell transformed, transfected or infected with the vector of any of claims 25 to 32.
30. An isolated nucleic acid according to any of claims 18 to 22 for use as a medicament.
31. An isolated polypeptide which is involved in a pathway for programmed cell death of *Candida* spp. and encoded by a nucleic acid as defined in claim 18 or 19, wherein said polypeptide is selected from:
- (a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a polypeptide having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632,

- 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732,
- (c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 434, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 718, 720, 722, 724, 726, 728, 730 and 732, and
- (d) a functional fragment of any of said polypeptides as defined in a) to c).
32. A polypeptide according to claim 31 for use as a medicament.
33. An antibody capable of specifically binding to a polypeptide of claim 30 or to a specific epitope of said polypeptide.
34. An antibody according to claim 33 for use as a medicament.
35. A pharmaceutical composition comprising an antibody of claim 33 or 34.
36. Use of an isolated nucleic acid encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396,

398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 589, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a nucleic acid encoding a protein having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 299, 299, 299, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 589, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(d) a nucleic acid comprising a sequence as represented in any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415,

417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(e) a nucleic acid which is more than 70% identical to any of the nucleic acid sequences as represented by any of SEQ ID NOs 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481, 483, 485, 487, 489, 491, 493, 495, 497, 499, 501, 503, 505, 507, 509, 511, 513, 515, 517, 519, 521, 523, 525, 527, 529, 531, 533, 535, 537, 539, 541, 543, 545, 547, 549, 551, 553, 555, 557, 559, 561, 563, 565, 567, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 731,

(f) a nucleic acid encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and

(g) the complement of any of the nucleic acid molecule as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

37. Use of an isolated polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from:

(a) a polypeptide having an amino acid sequence as represented in any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

(b) a polypeptide having an amino acid sequence which is more than 70% similar to any of the amino acid sequences as represented by any of SEQ ID NOs 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 569, 571, 573, 575, 577, 579, 581, 583, 585, 587, 589, 591, 593, 595, 597, 599, 601, 603, 605, 607, 609, 611, 613, 615, 617, 619, 621, 623, 625, 627, 629, 631, 633, 635, 637, 639, 641, 643, 645, 647, 649, 651, 653, 655, 657, 659, 661, 663, 665, 667, 669, 671, 673, 687, 691, 693, 695, 697, 699, 701, 703, 705, 707, 709, 711, 713, 715, 717, 719, 721, 723, 725, 727, 729 and 732, or encoding a functional equivalent, derivative or bioprecursor of said protein,

304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666, 668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732.

(c) a polypeptide having an amino acid sequence which is more than 70% identical to any of the amino acid sequences as represented by any of SEQ ID 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 299, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 324, 326, 328, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, 484, 486, 488, 490, 492, 494, 496, 498, 500, 502, 504, 506, 508, 510, 512, 514, 516, 518, 520, 522, 524, 526, 528, 530, 532, 534, 536, 538, 540, 542, 544, 546, 548, 550, 552, 554, 556, 558, 560, 562, 564, 566, 568, 570, 572, 574, 576, 578, 580, 582, 584, 586, 588, 590, 592, 594, 596, 598, 600, 602, 604, 606, 608, 610, 612, 614, 616, 618, 620, 622, 624, 626, 628, 630, 632, 634, 636, 638, 640, 642, 644, 646, 648, 650, 652, 654, 656, 658, 660, 662, 664, 666,

668, 670, 672, 674, 688, 692, 694, 696, 698, 700, 702, 704, 706, 708, 710, 712, 714, 716, 718, 720, 722, 724, 726, 728, 730 and 732, and,

(d) a functional fragment of any of said polypeptides as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

5 38. A pharmaceutical or fungicidal composition comprising a nucleic acid as defined in claim 36 or a polypeptide as defined in claim 37 together with a pharmaceutically acceptable carrier or a pharmaceutically acceptable carrier.

10 39. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid as defined in claim 36 or at least one polypeptide as defined in claim 37 in a pharmaceutically acceptable carrier.

15 40. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or the polypeptides as defined in claim 36, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified yeast or fungus.

20 41. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- (a) contacting a compound to be tested with a genetically modified yeast or fungus according to claim 40, in addition to contacting wild type cells with said compound,
- (b) monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to said wild type cells, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (c) alternatively monitoring the growth and/or death rate and/or activity of said genetically modified cells compared to genetically modified cells which were not contacted with the compound to be tested, wherein differential growth or activity of said genetically modified yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said genetically modified cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

42. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 5 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid as defined in claim 36, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 10 (b) monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 15 (c) alternatively monitoring the growth and/or death rate and/or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested, and,
- (e) identifying the compound.

43. A method of identifying compounds or polypeptides which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

- 25 (a) contacting a compound or polypeptides to be tested with at least one of the polypeptides as defined in claim 37,
- 30 (b) detecting the complex formed between the compound or polypeptide to be tested and said polypeptide,
- (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound or polypeptide being tested,

- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound or polypeptide being tested, and,
- (e) identifying the compound or protein.

44. A method for identifying compounds interacting with a polypeptide involved in a pathway eventually leading to programmed cell death of yeast and fungi comprising the steps of:

- 5 (a) providing a two-hybrid screening system wherein a polypeptide of claim 37 and a protein interacting with said polypeptide or an interacting polypeptide obtainable by a method of claim 41, are expressed,
- (b) interacting said compound with the complex formed by the expressed proteins as defined in a),
- 10 (c) detecting a second complex, wherein the presence of said second complex identifies a compound which specifically binds to one of said polypeptide or to said second complex, and,
- (d) identifying the compound.

45. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- 15 (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid as defined in claim 36 joined in frame with a reporter gene,
- 20 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested, and,
- (c) identifying the compound.

46. A method for identifying polypeptides involved in a pathway eventually leading to programmed cell death comprising the steps of:

- 25 (a) providing a two-hybrid system wherein a polypeptide encoded by a nucleic acid according to claim 36 or a vector according to any of claims 3 to 7 as a bait and a yeast or fungal cDNA library as a prey are used,
- 30 (b) detecting an interaction between said polypeptide and a yeast or fungal polypeptide encoded by said cDNA library, and,
- (c) identifying said yeast or fungal polypeptide.

47. A method according to any of claims 41 to 46 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

48. A compound or polypeptide identifiable according to the method of any of claims 41 to 47.

49. A compound or polypeptide according to claim 48 for use as a medicament.

50. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound or polypeptide according to claim 49 with a suitable pharmaceutically acceptable carrier.

51. A pharmaceutical composition comprising a compound or polypeptide according to claim 49 together with a suitable pharmaceutically acceptable carrier.

52. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or obtainable by the method of claim 50 for the preparation of a medicament for treating diseases associated with yeast and fungi.

53. A method for preventing infection with yeast or fungi comprising administering a composition according to claim 51 or obtainable by the method of claim 50 to a mammal in an effective amount to stimulate the production of protective antibody or protective T-cell response.

54. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a specific epitope of said polypeptide, for the preparation of a medicament for treating diseases associated with yeast and fungi.

55. Use according to any of claims 52 to 54 wherein said disease is associated with yeast or fungi, where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomycosis dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

56. Use of a compound or polypeptide according to claim 48 or 49 or a pharmaceutical composition according to claim 51 or a genetically modified organism as defined in claim 40 for the preparation of a medicament for modifying the endogenous flora of humans and other mammals.

57. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof or at least one of the polypeptides as defined in claim 37 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents, delays or sensitizes for apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

58. A genetically modified mammalian cell or non-human organism according to claim 57 wherein said modification comprises the expression of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid.

59. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acids as defined in claim 36 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 37 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 57 or 58.

60. A compound identifiable according to the method of claim 59.

61. A compound according to claim 60 for use as a medicament.

62. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 60 or 61 with a suitable pharmaceutically acceptable carrier.

63. Use of a compound according to claim 60 or 61 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

64. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

65. Use of a nucleic acid selected from any of the nucleic acids as defined in claim 36 or a human homologue thereof for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

66. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

67. Use of an antisense molecule to at least one of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian homologue of said nucleic acid for the preparation of a medicament for treating and/or preventing and/or alleviating proliferative disorders or for preventing apoptosis in certain disorders.

68. Use of a polypeptide selected from any of the polypeptides as defined in claim 37 or a human homologue thereof for treating and/or preventing and/or alleviating proliferative disorders or for the prevention of apoptosis in certain diseases.

69. A pharmaceutical composition for use as a medicament for treating proliferative disorders of
5 for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as
defined in claim 36 or a human homologue thereof or an antisense molecule to at least one
of the nucleic acids as defined in claim 36 or an antisense molecule to a mammalian
homologue of said nucleic acid or a polypeptide as defined in claim 37 or a human
homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient
therefor.

70. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid as defined in claim 36 or a human homologue thereof or at least one polypeptide as defined in claim 37 or a human analogue thereof in a pharmaceutically acceptable carrier.

15 71. Use of an antibody capable of specifically binding to at least one of the polypeptides as defined in claim 37 or to a human homologue thereof or to a specific epitope of said polypeptide or said human homologue, for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

72. An expression vector comprising a nucleic acid as defined in claim 20 36.

73. An expression vector according to claim 72 which is an expression vector wherein said nucleic acid sequence is operably linked to one or more control sequences allowing the expression in prokaryotic and/or eukaryotic host cells.

74. An expression vector according to claim 72 or 73 which comprises an inducible promoter.

75. An expression vector according to any of claims 72 to 74 which comprises a sequence encoding a reporter molecule.

76. A host cell transformed, transfected or infected with the vector of any of claims 72 to 75.

77. An isolated nucleic acid comprising a human homologue of at least one of the nucleic acids as defined in claim 36.

30 78. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 77.

79. A polypeptide encoded by a nucleic acid of claim 77.

Figure 1:

YBL002w, 896 bp, CDS: 501-896 (SEQ ID NO 21)

TGTTTGATATATAGTAGTCATGTTGTTAACTCTGGCCCTAAGTATACGTACGAAATGGTAT
GCATGTCGCGTTATTGGCCCGCAGGTTAATGTGTTCTGAAATTTGECATCACCTTTGAGA
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CTCAAAATTTCTCCCGTTTTCAGGATCAGAGCGGCATCTAGTCTGTGTTAAATGGCGC
TTACAGAAGAACAGAAAGAAGAACTGCGCTAATGCAACAGTAGAGACATTTGCCGCTCATAT
ATAAGTTTTCGATCAGTAAACCGTTAATTTGAGCATTACACAGGTTTAAATATATATTT
ATATATCATGTGATGTAAATATTTTTTTCGTGACTGTTTGTGTTTATTTATTTAGCT
TTTTTAAATATTTTACTTTCCTGTGTTAATTTTTTCTGATGCTCTATCTCAAAACCAAC
AACAACTTTACTCTACAACTAATGCTCTCGCCGCCGAAGAAACAGAGTCTTCCAAAGCTC
CAGCTGAAAGAGCGAGTCCCAAGAAACATCACTCCGTCGATGTTGAAGAAGAT
CTAAGTTTAGAAGACATCTTCCCTATATTTATTTACAAAGTTTTCGAGCAATCCACC
CAGACATGTGTTATTTCCAGAAAGTCTATGCTCTATTTTGAACCTCTTTGTTTAAACGATATCT
TTGAAGAATATGCTACTGAAGCTCTTAAATTTGGCCGCTTATACAAAGAATATCCACTATTT
CTGCTCAGAGAAATCAAAACAGCCGTTAGATGATCTTACTGCTGAATTTGGCTTAAACATG
CCGTTCTCAGAAGTATCTAGGGCTGTTCCCAATATCTCTCTCTCTCTCAAGCCCTAA

YBL002W, 131 aa (SEQ ID NO 22)

AVTKYSSSTQIA
KSMISLNSFNDIFERATEASKLAAYNKKSTISAREIQTVRLILPGLAKHAVSECTR
MSSAAEKPKPASKAEPKPAAKKTSTSDVGKRSKVRKETYSSYVYKVLKQTHPDPTGLSQ

YBL064C, 1286 bp, CDS: 501-1286 (SEQ ID NO 25)

TTGCCAACCTCAAAGAAGAAGAAATTAATGGGCATATTATGACACTTCTCCGGTTTCCCTCCCGC
GCCTCTGTAATCCGCTCGATTTGACCTCGAGCAAGCGCTCCACTATGTCGTCTATATATGTTTAC
CGTAATAACTCTTTAACTGTTGATATTTTGTAACTTTCAACCACATTCAGTATATGCGGTCA
TGTATAAAGAATATCTCTGTATAGCACTATGTTTATCTTTATACAAATTCATAAAGGTCG
CCAGAGACGACAGCGCGCTATTTTCTATCATCTCCGTAATATAGCGACCAACGGTCGGC
GGCTATTTTTTTTTTTTGGCAATTTTTTTCGGATGGTTCCTCCGCAAAAGCTAGACCCCGGA
GATTTTAAATATACGTATGAAGAAACAAGAGCCCGATTTGCTGCTATTTGGTATATATAAGAG
AAGAGGAGAGATATAGAATAATTTGTGCTCTAGATTTCTCGCAGTATAGATGAGATAAATTTTC
AAAGACGAGGAAGCAAGAGATTTTGTATGAGAAATTTGTAGCGCTCAATATAGAGAGACGG
CATGACCCCTTCTTAAGCAGGCTCACTTGCATACACAGAGATTAAACAATTTGCGCACAG
CACTATTTCTGTGCAACAATTAACAAGATGATCAACAAGACATAAGATAAATCTGT
ATGCTCTTAATCTTGATGCTGTGACAAACGGTTGGTTAAATATCAATTTTTTACGACTACTTGG
CGCACTCTTTGGGGTCTTTCTCTACCCACAGATTTCCACCCCTGTCGACCAACACCG
AAGTCAGCGCATTCGCCAATTTGAAGCCGGAATTCGACAAGAGAAATGTTAAATTTGATCG
GGCTTTTCAGTGGAGAATGTTGAGTCCCAAGAAAATGGATTCAAGACATCAAGGAAATAG
CAAAAGTTTAAAAATTTGGTTTCCCAATTAATTTGGTGAATTTTATAGAAAGCTGGCATTC
TATATGATAATGATATGCCCGAAGGATTAATAAATATCAATATGATGGGTCACTGAAGACCG
TGAGGTCTGTTTTGCTCATGATCCCAAGAGAAGATATAGACTGATTTTATACCTACCCCTT
CCACCGTCGGAAGAAAACACTTCTGAACTGTTAAGGTAATCGACGCCCTTGCAATTTGACTG
ACAAGGAGGCGGTAGTAACTTCAATTTAATTTGGCAGCGAGCTACGATGCTATATTTCTCT
CCTCTGTCTCCCAATGATGAGCGAAGCTAAATTTTGGTCAATTTTATGAATAATTTAAACCTT
TTTAAAGATTCACCAAGTCGAATAA

YBL064C, 261 aa (SEQ ID NO 26)

MF\$R1CSAQLKRTAWTLPKQAHQSQITKTFATAPILCKQFKQSDQPRLRINSADPNFAD
DTTVGKINFYDYGDSGWGLFSPHADFPVCTTEVSFAKLKPEFKDRNKKVLIGLSVEDV
ESHEKWTQDIKEIAKVRKNGPPIIGDTRFNRAFLYDMVDAGFPKNINDGSLUKTVRSVFV
DPKKRLIFTVPTVYKRGTSVLRVLDALQTDKEGVTPIWQPADDTIIPPSVSINDE
AKAQFGFNEIKPYLRFTKSK

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YBR289W, 905 aa (SEQ ID NO 64)

MNQPGOTNSVPNSIGNIFSNIGTPSPFNMAQIPQOLVQSLTPQQLMTQQRHQQLLRSLRSL
 QQQQQQQQQQTSPPTQHQSPQPPQSQPTANQSATSTPPPPAPHLNHPQIGVPLAPLA
 PINLPQIQLPIATQQQVLNKLQQAIAKNNQPVNNAITVAQQQVQRPQIEQQQQQQTAQ
 TQLEQORQLLVQQQQQQLNQRIQRQQQPHHVQI1Q0000K0000Q0000Q0000Q000
 Q0000000000000000000000000000000000000000000000000000000
 LPKLNPKYQITQVDPPETKLPVTVYWSKKADTD7LLYEQI1QORDKINKYSLIRETWGY
 DFFSYVGSNKEYISRWMLHYTKYVQDUKUNTRMKSITSQKIPSPASWGNQVSGVNGGIT
 NTRTVIPOVEGVNGNHLLEDKLYKVAQANNETSEQLVP1RLPEFDQDRDFRLRTLWN
 KMDKLK1EDFVDDMLRDYRFEDATREHQH1DTCISTEQIEQGNPVIENLDORLGD
 DLIRIKLIDLWQGNOLIQDFEWEINSNDNCPEEFAESMCQELBLPGFVTAIAHSIREQ
 VYNYHKSLALLGVNFQGS1EDDDIRSMPLTT1LDVDPYPAAESKIF1TNLLQISAAEL
 ERUKDKODRTRKRGNSRGMGLASCTASNTSMGVNTHVTAAGNSSLPPGELL
 PDIAD1PRTFRTPV1PSTLMPGVDGVSVESYELRNTTYYTRDRPKVPSPPCVYIDH1
 PGHSLLSTKLPGKVNTEKFAAANPD1TSGTNAMLPSPESLKTKLNSNIRAGVTYIP1P
 NPIANHVTNSNP1TQV1PFGAA5KSVPTP1SLPTAPPVAPHDSEATL1TN1NNGSSNN
 N1ANTNT

YCR004C, 1244 bp, CDS: 501-1244 (SEQ ID NO 69)

[illegible]

YCR004C, 247 aa (SEO ID NO 70)

MVKIAIIITYSTVGHIDVLAQVKKGVEAAGKADIVRYEETLPDEVLTQMNAPQKPEDIP
VQETKTLLEYDAFLFCVPTRFEGNLPQAWSAFWKTGGLWAKGSLNGKAAGTFFVSTSSVGG
GQESTVACLSYLAHHGIIFPLPGYKNSFAELASIEVHGSGSPWAGTLAGPDGSRITASP
LELRIAETQGTIFYETAKKLFPAKEAKPSTEKKTTTSDAAKRQTKPAAATTAERKEDKGL
LSCCTVM

YCR013C, 1148bp, CDS: 501-1148 (SEQ ID NO 77)

[illegible]

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AGATAAATAAATAGTCTATATATACGTATATAAATAAATAAATAATATTCAAAAATAATAAATAA
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AATTCATTTCAATTTATTTCTTTGGATATAGAAAGCAACACCTGGCAAATCTCTTACCTT
CCAATAATTCAAAAGCAACACCAACCACTAGTAGAGATCTGGGAGATCTTGTCTAGTACAC
CGTACTCTTAGCGACAGTGGCAGTGTACCAACCAATAGTGTACGGTGTTCACGACG
CAGAGCTCTTCGACAACTTGTCTAACAAAGCCTTAGTACACGACGGCACTTTTCGAAAT
GAAAACACTCTGTGGACCGTCTTCAGACAAATGTCTTAGCCTTTGCAACAGTAGCAGCA
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CTGGCAGAAGCACTTCGACACCCCTTGTGGCCTTTGGCCCTTTTCATCAACTTTGGAAAGCTGA
CAGCACAAGCCTGTGCAAGATGGAGTACCCGATTTCAGTGTTTTCCAAAAACCTTCTTGA
AGGTAAGAGCCATACCAACCAATGATAGAGTCGACCTTGTCCCAACAAAGTGTGCA
TCAATTGA

YCR013C, 215 aa (SEO ID NO 78)

MGKEKRKLLIYRFNFSTYFSDKKATCGNSLPSNNKCAPPEVETWELISVTPYPLATV
AVSPFPMWTVLPAAEELIUTSSNKALVPAANFSNKTPGGPQTWLAFAVTAANNFLDSG
PLSNPCQAPGISVTVLVLASAEKASAMKSTGKTTPLALAFISNGFTISAPALSK
MESPIVSVFSTKFLKVKAIPPPMMIESTISNKLIN

YDL059C, 1217 bp, CDS: 501-1217 (SEQ ID NO 83)

AAAGTATCAAGTTCGCTAAATTTACTTCGAGACAGAAAGCCAGTAATTTTGTTCCTTCG
ATGGAATAAGTTTCCAAAAGGTTCTTAGTAATTTACCATAATGTTCTGTGATCTCGCGCGTCG
GAAAGAAAGTTAGCGGACCGCATCCCATTAATTTGTTATATAATAGCAATAGGAACAAT
TGTTGAAGTTTCTTTAAAGCTATATAGTATTCGAATATATCAATGTTCTACCTTGAATAAT
TGGGTATTTTATGACCAATTAATCCGCTTGGACACTAATCTTTTCAAGTTGGTGTCAC
GTCAAGTGCTTTTCAAATCTACTGGGCAATTTGATATAGAGAGCCACAGTTTGGCAAGG
GCAGATGATAGGAAGCAGTAAAGCCAAAGGAAGTAATAGAACATCATTTGGAGGAGTCTG
TGCAGTTTATAGCAATGCTTTTGAACCATTAAGAAGGTTACTAGAGGAAGAGACATATTT
CAGGATAAACAGACAAATAATATGACGATACAGCAAGCCCACTTTCGAGCAATATCGTATG
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ATTTGGAATGAAGACCTTCCACGCGCTTGCTGGCTGCAGAGGATTTGGGCTCTACAGTCCA
AGAATGAAGGTACACCTTACATATTTTCCACAAATAATTAATTTGGGAAGCAACAATTTAT
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GTTTGGCGAATAAGATGTTTATAGATCTTGAGCGCCGGAGTGCACGCCCTTCAACCGCATAA
ATAATGGAGAAATAACCAACACTATAGTAGGTTCAAGTATACATGTTGGCAGAGAGCCCAAG
TAAAGGTACTTTAAAGSATGCAACACACATGCTTGCTGGCGTAGGTAGAAATTAATT
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AGAAAGCGTTATTTGAGCTTTGAAATAAATCTACTCGATTAGAGACTTAGAGATTACAAATA
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ACCATTAATGTCGACCACTAATAGCAAGCCGACTTTTATCAAAATTTGGAGGATGCTTAAG
GCACCGATATCAATAATA

YDL059C, 238 aa (SEQ ID NO 84)

MTIQAKPSSISVSDSTTYGTAPGLDIKEFQIIEDNGRCPASAWSQIRIGLLQSKIERTY
NIYHNKYGKHNL SKLIPGHALIQANETFGYDGRMDVDEARECOPFTAVNNGENTN
TSEVXYTVAEAOVKVTLKDGNTQCGGLGRITLSRGECYNRSKKEAVGDALKALLSF
EKILLDYETKITNNYYDGLYGSKKIKNEANTYNLLSATNKSPPFTIKLEDAKSTHTK

YDL147W, 1838 bp, CDS: 501-1838 (SEQ ID NO 87)

ACTCTCTCTGATTTTCAGCAATGGCCCTTTTTTTTCTTCAGATCATACTCTCTTCGCTT
GTCCTTTGGAAATCTTTTTTCTTACTTTTACGTTTGTAGTTTGTAGCTGTAGTGTCCAGGG
CCTTCAAGCGCCCTTTAAATCTTAAAGTTGTGACCGGCACTGATTTGATCTTCCCTT
TTATTTGCTTCTCAACGTACTATTTACAGTAATAATTGCAACCTTCAGATGCTTCT
CGTAATAAGCTCATCTAAATCAATTAATTTCTCTTAATAATCTTAAATCTTAAATCTAC
TCGTTCTGTACGGCTCATCGCCCAATTTACCGCTTGTGTATGTGATCTTTTGTGATCTT

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>YGR034W, 1244 bp, exon1: 501-525, intron1: 526-879, exon2: 880-1244 (SEQ ID NO 169)

TATATAAATAATCTTGTAGACATATAAATAAGAAATGCCCCATTTCTTAACCTACCGGAAA
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GGAAATTTTCATAGTGTACAGTGTAGGATGGTGTCTAGTAGAGGTGGCGCGGTGA
TGGGAATTTCTCATAGTTTACACATAGTGTGGAAATTAATAGTAGCATAGCTATC
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GCAAGCAAAAGATATATAATTAATGGTGAAGCAATCTCTAGGTATGTGTGGAGGATAG
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AGAGAACAATTAATGAATGTAAATTAATGTAAACAAATGTATGATAGAGGAGA
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GGCAACATAGATTAAGTGTGGATGAATAATTAATGTGCTCATTTGTGAAAATAAAGTTTG
CTTTACTAACAATTTTATTAATTTTGTCTCAATAGACGTTTCTCTGACAGAGAA
AGCCAGAAAGGCTTATTTCACTGCTCCATCTCTGAACGCTGTTTGTATTCGCTC
CATTTCAAGGAATTGAGAGCTCAATATGTAATCAAGGCTTTGGCCAAATCAGACAGAG
ATGAAGTCTTGGTGTGCTGCTCAAGAGGCTCAAGAGGTAAGATTTCACTGTTT
ACAGATTGAAGTTTGTCTGCTCAAGTTGACAGGTCACCAAGGAAAGGTCACCGGTGCT
CCGTTCGAATTAACCTGACCCATCAAGCTGTGTAATCAATAGTTACACTTGGACAAGG
ACAGAAGGCTTGTATCAAAAGAAAGGTTGTAATTTGGAATAA

>YGR034W, 129 aa (SEQ ID NO 170)

MLNYCKTWYSSDRRKARKAFATPSSSERVLLSAPLSKELRAQYGIKALPIRDRDEVLV
VRGSKQEGEKISSYRLKFAVQVDKVTKEKNGASVPINLHPISKLVITKLHLDKRKAL
IQRKGGKLE

>YGR069W, 836 bp, CDS: 501-836 (SEQ ID NO 171)

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TTTCGGCATTTTCCCAACGACTTAAACATCCCTTTTGAAGAAACCAATAGTTGTCTCC
ATAAGCATTCGAAATCTTACGCTTTTCTTAACTTATAGACTTGGCAAACTGCTGCTTCT
TCTTATATCGGCCAACTTGAATCTCAATTTGAATCTCTTACCAATCTCTACGCGAAA
TTTTCTTCACTACATCTATTTTCACTGAAATCACTAAGTTTCTGATAAAGGTATAG
ACGACAGTTCCAAACGGTACCTTGGATCAAAATTAATGCTTGTAGCGGAGCTTATTC
TAATATCAAAATAACTTATTTCTCTCTTCTTCTCTGCTCTGTAATGCCACCGCTGTAG
ATAGCAACTAAGTGAAACATGTGCTTCTTACCTTACCTTCTCGCGGAGAGCTGTACAA
GATATTTTCTTACTTTTGGCCATCTTATACATCACTCAATCATCTGTTTCTTCTTCTA
TTTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTA
GAAATGTAAGACGAGTGAAGTATTCAGGAGTATTAATTAACATACATACAAAGCAAG
ACAAAGAAACATTTTATAGATCTCAATTTTACTTCAATTTTGTGATTTCTTTATATA
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>YGR069W, 111 aa (SEQ ID NO 172)

MVLLHPILAESCTRYPLLLPSYTHNHLFHPFSISFFFFFRRNCLPRIVKDEV
KYSGVYVYHTKQDKETFLDLTFTFVNCFCIPYKNDLLLFNVGVIRPLLDLQ

>YGR070W, 3968 bp, CDS: 501-3968 (SEQ ID NO 173)

AAGAAACATTTTATAGATCTACATTTTACTTCAATGTGTTTGTATTTCTTATATAAGA
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CGATTTTCTTCAAGCATGCTTGTATGTTTCTTAAATTTCCCATGATTTTGTGCTG
CAATGTGATCTTACAAACTATACAGAAAGTAACAGCACTTCACTCTTTTGTGCCCTAAA
ACGGCAATATTTAGACATATCATAGGGGCCCAAGGGAGAAATCGTTAAATTTTAAACTTTT

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CTTTGCTCTTGAATGAATAAAGTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
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GCTCAAAAGTTTCAAGAAACATCAATGAATTTCTATCACTAAGCATGAGGATGAAGATA
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CACGCTTAGGATAGACCGGCTTCTTCCCAACCAATTAAGAGCATCTCCTGCTGCTGAC
ATATTTCAACAAACCTTAATTAATCAAGTCCAATCTCTTCAAGGGCATCAGATTTTCACTTA
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GTTATTTCTCTACATGCTCTCTGGAATAAATTTGTTGCTACTCTATTTCTTGTCCCAATCTT
TGCACCAACAGGCTTAATTTTACATTTAAATTTAGTGTGTTGTTTGTGCGATATCTCTCTT
TAGCACTCGATAGGAGGATGATGAACGAATTTCTTGGACAAATTTCTGTACCAAGAGGG
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TTGATCTCTTTCTGTCTACATAGCATCAAGCAATACAGCAATCTGTACCAAGAGGG
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TAATGAAGTCCAAAGATCTTTTAAAGGATCTAATGAAGAAGATTTCTATTTCAAAAATGAAT
CAGCAAGAATCTGTATGAGTTTAAAGTGTAAAGCAGAAAATTTCTATTTCAAAAATGAAT
ACGTTAATCTGGTGTGAATTAACGAAAAGGAAAATTCAGCATGAAGGTTTACTCTCAA
GGAAGGCGTGAACAAACAGATGCTCTTTTACAGGAGACATTTCAATTTTACTCTCAA
ACAATATGCTAATTTCTGTAAATCAAAAGCTGTAAACAGTGGCACCACCAACACACTGTAT
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TAAAGAGATGTGACAGAAAACCAAAATTTGCTCAGGGGTGCTCTTACCCCAATATC
AAAGCAATTTCCAGAAATGCTATTTGATTTGCTTATTCGCTTATACGGTACGAAACAAATATC
AAGTACTTTTGTGCGCGCGAGCGCGGATTAACAGACATTAATAGAAAGGTGAAC
AAGACAAAAGGCTCTTGTGATGAACATAACATATACTTTTAAAGCAATGGTAGGTC
AATTTCTTCACTCATACATAAATATACTAATCGGCTCAACGATGCTCTAATCTGTCTGCTG
GTAAATTTTATTTGGTGTGCAACAAATATGGGACTCTTTGTCTTAAATTTATGCTATGCA
TCAATCAAAACCGCTGACCTTCTGACACAAAATAATCAATTTTACAGATCTCTGTATTTGG
AAGATATAAAGTTATGATTTCTTAAATTTGACAAAACCTGTACGGCTCTCTTTTAGAGC
TAAATCGAGATGACAGAAATCGAGATTTTCTTTTCAGAAAAAATTTCTAAAGTGTATTTTA
ATCATTTTGTGAATTTCTCAAGAGCGGTTCGTAAATGTTAAAGAAATCATTTATGATTTGCA
ATCATTTTGTGACCGCGCACAAATTTATGATGTTTAAATCTCTTGTATTTTCAATTTTAA
GGGTAAATTTTAAAAAAAACCCTTAAAGGCGGCTTGGTAGATTTTGGGCTGTGATTTCTGAC
CTCTGCTCTTTTCTTTTTTGGAGAAATAGATCTGCAATTTGTTGTTGTAATAAATAATCAAAA
TATTAAGTACCGGAGTGTGTGATATAAATTTGATTTTAAATTTAGGGAGCTTTTAAATCT
TACATGATCAACAAAGTTTTAGGACATGATATAAAGAGGCTTCAAGTAGTGTTCATCT
TTCCGATAAAAAATTTTCAACTTTTGTGATGTTTCTTCCAGAACTCTGCTCTCAATAAGC

ATPAGAGCTGATATTCACGTGACTACAAAGTGTGAGGGTATTTGGTTATGATTTTGTGTTCTTCAGAG
TTTTGGCAGAGAAAATTAATTTGATGTTTGGTATTAAGACAGACGACAAAGCCTTCTTTTCAAAAT
ACGCCAGACAATTTGATTTTAAACGAGGTTCTTTGGTGGGTGCTTTCTCCGGTTGTTGCTGCT
TCACTCGGGTGTGAAATACACTGTGAGACACACCCGAACTGACTGACTGAGATGATGTCAATTTG
TTGCCATATTTCCAGATTCATCAGGTCGTACCTTAACCAAAATTCGTGATGACGACGAATGGT
TGAAAAGNACAATTTGTGGGATGAGCTGTGTGGCCGTTTGTGACTTCTTCAAGAGCTGG
AGGCTTTGCAGACAAAATACGTGATGTTTGGTATGACCGTACTGTATTAAGGATCTTCACT
TGAAACCGGTTGTGTTCCGTTTAAGGAAACCCGTAAGGTCACGTATGTTATCAAGATATATTA
AAGACAAATGGCTTTGACCAATTCGCTGTGTGACTGAAGACGGCAGGTGTCTTGGTTTAG
TTACTCTCTCAGCTTTGAGAAACACTATCAATCAATTAATTCACAACGACACACTA
TAAGGGTAAATACCTTTGAGCTTTCAAGAAATTAACAATTAATCAATGTGTCTCTCTTACA
ACGAAAATTAATCCCGTAAAGCAAGTTTATTAATTAATTCGATGAAACATCAAGGCTATCTG
ACTGAAATCGTTTGTGAAAAGAACTATCTTCCGCTTTTACGATGAGTGTGAGAAACCA
TCCATATTCGTTACTTATGATGGAATTTACTGAGCTACTTAGCATAA

>YGR155W. 507 aa (SEO ID NO 182)

MTKSQOADSRRNVLDVGNTPILIALUKPKALIGIKPQIYAKUELYNPGSGIKORIAKSM
VEEASGRIHPSRSLIEPTSGNTGIGLALIGAICYRTITLPEKMSNEKVSVLKALG
AEIIRTPAAANDSPESHGVAKKLEKEIPGAVILDQNNMNPAAHYFGTGREIQRQLE
DIANFDNLRAVAGAGTGTSIGISKYLBKQNDQIIVGADPFQCSILAQPENLKRITD
YKVEGIDYFQVQLKIDMWTDDKRSFYARQLISNEGVLVSGSSGSAFTAVVKY
CEDHPELTEDDVIIVAFPPSIRSYLTKFVYDDEWLKKNLWDDDDVLARFDSKLEASTTKY
ADVFGNATVKOHLKPWVSVEKTAFTVDITLKLKNDGFDQLPVLTEGDKLSGLVTLSELL
RKLSTNNSSNDNTIKGVIYDFDKXLAMFNDSVSSYNEKSGKKFKTKFDENSKLSDLNRFPE
KNSSAVITDGLKPIHIVTMDLILSYLA

>YHR095W, 935 bp, CDS: 501-935 (SEO ID NO 207)

GACACCTTTCCGGTGTGAGAGGGGCAACGGCGGGTTGCATCTTGACCTTTCACCTTAAAGTT
GTCTGTAACAACCTTTCATCTTTTACCTCTCGAGTATATCAATGCGCTTTGCAACGACAGATTC
CATTCATATGATGTGGATTAATTTGGATTTCTGAGGAGATATATAGATCGGGAGTTGAATTC
CAATGATTTACGTATATCAATAGTTTACGATCTATGATATCTTTATAGATTTTAAAGTGTGG
GGAAGAACAATGAGACCCAGATGGAAATGTGATATGGGGACATTTGTGGCCCTTATATATATA
ATGTAATATTTGCTACATATAGATTAATGGTGGAGTTCTCTGGCTGTGCGGATATAAAGCGCA
TCAAAATGTCGACGACGTACATGATTTAGTTTGTCTGTCTCTGCCCATGATTAAGATTCG
TATTTCTTATACGACACTTGAAGAAATATCTTTTTTCTCATATATCTGGAAGACAATAAGAT
CGGACGCGCAATGCCCTCGACAGATCTTCTCTAGTTTTTCCGAATTTCCATATTCAGTATATG
CAGATCTTGCGGATATTTGTCTAGCTCTTACGGAATAAAAAAAGAGACGTCCGGTCTCACTT
CGGAATAAATCTTGTACTATATGCAACAGCAATAATCTTTTGGCGTCTCTCTTTGAAGA
AAATATCAGAGTGCAGATATCGATTAATTCCTTTGGAAGTTATGATGGTTAGTCTTATGTT
TAACTCTCTGAAGAAGGGTTTTCAGTTGGTCAACAATCTTTTAGAGAGTATAAAAAAAA
CAAAAAAAGAGAGATTTCTCTATATTTACCATGATCTTACGTTTGTGTAAG
CAAAAAATGAAGATATATCCGAGGGCGATCGGAGTAG

>YHR095W, 144 aa (SEQ ID NO 208)

MWLFLIYLDKDKRSARQCPAALPSPSEFFPLRIGCSAHIQCSTFERKKEHWVTSEKLLITQ
 CNSVIIICAVSLKKNQCKISINSLEVMVWSLSITLLKKGFFSNSTLFRGKKKKKKKKKKR
 ILHVYHDPSTELQAKKTIIRANAK

>YHR138C, 845 bp, CDS: 501-845 (SEO ID NO 209)

CTACGAAATTAAGCAAAAAAATAATTAATAAACAACAAAAACAACAAACAAAC
AAAAACAAAAACAACAAACATAATTTATATGATCTGACGAGCAAGAAATCGTCGTGA
TTCTCCATAATTTGTCCTCAGTACATATATCTGAGTCTCTCTCTTTTATATG
ACTATGATGATGTAAGTACATACACGGCTTCCTTATATGTTCTTTTTTATGTCGT
TACAGGATTTATGTTTATAGATATATGATCTAATAATTTCTAATATTCATGTCGTGA
TTAAATTTGATTTATTTCCGATACATCGCTCGGCTCAACAAAGACGCAAGAAAG
TAAATTTGATTTATTTTATGATTTATGATTTATGATTTATGATTTATGATTTATG

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5'AGTAA
GAAAACGCAAGTGGATAAAGGGGTGGGGGCAAAAGATTTTAAAGAAAAAGCGATGCGGATG
GAGAGAACAAATGGATAAGTTGCGGTTTCCCTGTTATATTTACAACATTTAAATCTATTCTGTG
TAAACAGCATATGACATATATTAAGAGCGCATCTACTGTTTGTATTTTTCATTAGCATAT
TCTCCATGGCACAAGCATCTCCCTTATCATCATACATCTAGCTTAACTTTTCCCCACAAGGATTA
ATATGTGCTACGGACAGCAATAGCATATTTGAAGATGTCTAAAAATATTTGGTGAGCATAG
GGGTGAAAATTAACACACAGATATAGCTTGATTAAGGGGCTTTACAGTGGACTTACCTGATTA
CGACACAAATTTTGGAGCGCTGTGAAGAAGCTTTGAGCTATATTTGAAGCGGAGTACCGGTG
CTTAGTGCAAATTTTGGAAAAGGATTCAGAAAGTTCTATGCTCTTAAACCCGTGACCATTTTAGTTG
CTTAG

>YHR138C, 114 aa (SEQ ID NO 210)

MKASYLVLFISIFSMAQASSLSYIVTFPKTDNMTDQNSIEDVKYVVDIGGKTHE
 YSLIKGFTVLDLPDSDOI LDGLKERLSYIESEYGAKCNLEKDSVHALNRDHLVA

>YHR179W, 1703 bp, CDS: 501-1703 (SEQ ID NO 215)

ATATCTTTACGTAATGAACCTCTCGTAAAGAACTTCGGTAATTCGAAGATCTCTTTACGATCTCT
 TTGTTTCAATCTTTACAGCATCTACTAAGTGTCTTTACCAACGATTTGGATGCTCTATTTACAAAT
 GAATGAATATTTAGTACCGGAACGAGCGCATGCTTTTCCGTCTCGGTGCTCTTAGTTAA
 AGCAAAACGGAGTGAATCGGTGAAGAACTCTCTTTTGGGTTGGAAATCAATTCGCTATG
 TTTGGACACCTTTCTTTTTCGGTATTTGTTGGAGCACCGCGTTTCTTTTGGGTACTTTGAT
 GAGGTAGCAGATCTCTGGAACTGTCTTCTCTCGAGGTAAACCTGCGCTGTGTCTCTCTCTGT
 GACTTTCTTAAATATAAAAGGAAAGCAATATCTAGTTTTCGAGTATCTTCTTTCATACTT
 TATTTTCTTTATTTAAACCGTTCAGATATAGAATAATCAATCATATTAAGCTAAATATAG
 ACGTATATATAGTATCGAATATGCCATTTGTTTAAAGGACTTTAAGCCACAAGCTTTGGGTG
 ACACCAACTTATTTCAACCAATCAAAATGGTAAACAAGTAACTTTCTACACCGTCTCTGCA
 TTCTTCAATTCAGCTAGATAGTAGAGCCCAACATCTCAGGTAAATATTCACAAACAGCTAGGG
 CCGTTGATACTTACGCTCAACGTGCTCAAGACACGAGAACTTTGATATTCACTGAAGTAA
 CCTTTCCCTCTCAACTCTTGGGGTTACAGCAATGCTCTCAGGTATCTGTGCTCCGAAGAAC
 AAATTAAGAATGGACCAAGATTTTTCAGGCTTATTCATGAGAAATAATCGTTTCGATGGG
 TCCAATTAATGGGTTTCTAGTTTGGGTGCTTTTCCCAACGACCCTTGCTGGGATGGTTTGC
 TTACGACTCTCGCTCTGCAACGCTGATATGAATTCAGCAACAAGAGAAGAAAGGCTAAGA
 AGGCTTAACACCCCAACCAACAGATATAACAAAGGATGAATTAAGCAATACGCTCAAGAAGT
 ACGTCCAAGCTGCCAAAACCTCCATTTGCTGTGGTGGCCGATGGTGTGTAATTCACACGG
 CTAAACGGTATCTGTGTAACCAAGTTCTTTGGACCCACACATCAATACCAAGCAACCCATGAT
 ATGTTGATATCTATCGAAAAACAGAGCCGTTTCACTTGGAAAGTGTTGATGCAATTTGCTG
 ATGCTATTTGGCCCTGAAAAGAGCGGTTTGAGATGTCTCAATATGGTGTCTCTACACAGTA
 TGCTCTGGTGTGCTGAACACCGGATTTGTTGCTCAATATGCTTATGTCTTAGTGGTGAACATAG
 CAAAGAGAGAGCTAAAGCTGCGAAGCGTTTGGCTTTTGGTCCATCTAGTTTGAACCTCTGTGCA
 CCAACCCATTTTAACTGAAGGTGAAGTGAATACAAATGGAGGTAGCAACAAATTTTGGTTT
 ATTTCTATCTGGAAGGGGCCAATTTATAGAGCTGTGTAACCTTTGCTCTGCAACCCAGAAATTG
 TCAGAGAAGAGGTGAGGATCTCAGACAATTCATCGGTTACGGTAGATTTTATCTCTATA
 ATCCAGATATTTGGTTGCTGTTGGAAAAAGGGTACCAATTAACAANAATATGACAGAGACA
 CTTTCTACAAAATGTACGCTGAGGGGATATCATTTGACTACCCTTACGGTACGAAGAAAGCTCTTAA
 AACTCGGTGGGAACAAAATTTAA

>YHR179W. 400 aa (SEO ID NO 216)

MPFVKDFKPBQALGDTNLKPKTKIGNNELHLLRAVIPPLTKRAQHPGNI PNDRWAVEYYAQ
RAQRPGLTIITEGTPSPSQSGDNAPGISEQIKEMWFKPKAIHENSFAFWQLWVLG
WAAF PDTLRAQYDASDSDVYMMWAEQBEAKANNPOHSITKTDKELQYVKEVYQAQNI
SIAAGADGVEIETHSANGYLLNGLDPSHNNRTDEYGGSIENRTFTLEVDVAQDAIGPEK
VGLRLSPGVFNMSMGGAETGVAQYAVYVGLGELREAAKGLAFVHLVEPRVTNPLFTE
GEGEYNGSNNKFAYSIWKGPIIRAGNFALHPHEVREAVDPKPTLIGVGRFFISPNPLVDLR
LEKGLPLNKYDRDFTFKYMSAECYIDPYTVEALKGLGDWNK

>YIL074C. 1910 bp, CDS: 501-1910 (SEO ID NO 219)

TCGGAGTCTTTAGCAAGTTCGGCAATAATCGATATCAATAGTATTGCTAAATAACCTTT

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TTTATTCACATTAACGTGCTTATACGTGACCTCTTAATTCCTTCAGCAATCTTGGCT
GCACCCGTCACAGAAAGCGTATGAATCGGTAGCTACAAAATTTTTCAGATTTAATA
AGTGCATATGTTTTCATTAATGTCACGTCATCTCAATTAATATACCTTGTCTTGG
CCAAATATACAAAATGCAATTTTTTCTTACACGGAAGATTTGGCCGTACCGCG
GACAGGCTACATTAATGCGGTAGATTCCTTCACGCTGGAAGACGTACACCTTATG
AAACATTAATGAATCTCCAGGTTTAAATACATGAAGATTGAGCTACATTAATAA
AATCTTCTGCTTGTAGCTAGATTAATGTATACATTTAAAGTACAAACATCTGAT
TCGGGTATTTCTCCCTAACATGTCTTATGACGTCCGATTAATCTCAACCTACATCT
AACGTGATGACCTTTCTGCTCTCTCTGTCAGTCTCAACCTCACCACATCTGAT
TTATGAACACATTAACCTGCTGCTGATGAACATTAACAACCAACCAAGGCTTAAACCT
TTCTACCTGCTGACATGAATATTTCTAGCTGTTGAAGATGCAATGCACTGATTAATA
TTCTTCAAGATTCAGGTTTACCAAGAGTTTCCACAAGCTTCTTACCTGACGATGAAT
TGATGAAAAATACAAAGACGTACACGCTATCGTATTAAGTCAAACTAGATGACGT
AAAAAATATACAGATGCCAGGATCTAGTTGTATGTTGATTTGCTTTTCAATTCGCAATCT
ATCAAGTAGACCTTAAATATGCTGCTGATTAAGTATGCTTTTCAATTCGCAATCT
CCAATTCAAGTCCGTAGCAGAAATTTGTAATGAGATCAATTAAGTTTGAAGACAAAT
TAGGTGATGATCCATGATGACATGACATGACATGATGAATTAAGTCCGCTGCTGAT
GGGAGTAAAGAGAAAACTCTCGGATTAATGAGTATGATGATGATGATGATGATGAT
CAGTCTTGGCAGAAAGCTATGGGCTGCAATGCTATTAATGATTAATGATGATGATGAT
CTTTAGGTACTGCGCAGAAAGTTTCAATTAAGTATGATGATGATGATGATGATGATGAT
TAAACATACATGATACACACTACTTCCAGAACTGAATAATTTATGCTGCTCCACAAATTCG
CTGCTATGAAGAGAGGGGCTTATGTAATTAATGCTCAAGAGGCTGCTTATGATTTATTC
CATCTGATGCTACAGCCGCTCAAGGCCAACAAATTCAGAGTCTGCTTATGATTTATTAATC
CAGTGAACAGCTTAAGAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGGTAAGG
CTGATGAGTTTCACTTACCAATTAATATCTGACACCAATTAATGATGATGATGATGATGAT
AAGCTCAAGTTCAATCGGATTTGAGTGGCTACTGATGATGATGATGATGATGATGATGAT
GTAATCTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAGAAACACAGTACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTAATGATATCTTATCCATCAATTAATGAGAAAGTTTTCGATGATGATGATGATGATGATGAT
TCGTTATCTATGACGACATCTCTCTGCTATCAAGTGAATTAAGATTAATTAATGATGATGAT
AAAAAGTAAACCAACTTCTGCCAAAGTTTCCATCAAGTATTAATTAATCA

>Y1074C, 469 aa (SEQ ID NO 220)

MSYSADNLIQDSFORAMNFSQVPEAFHKSIPEDLEIKIDVHAIGISRTLEKIDHA
ILLENVNAITAIKIPDQGYVEFHSKSPEDLEIKIDVHAIGISRTLEKIDHA
RNLVCIQFCIGTNDYDLRYASKGLAVENSPTSNSRVAELVJGEIISLARQEDRSIE
LHTGMWNVAAACWEVRKTLGIIVGHISGLSVLAEMGLVLYDVIIVIMAGTARQ
VSTIDELNKSDFVTLAVPATPEIKLSAPOPAMDGAVVINAISRGTVVDIPSLQAV
KANKTAGAALDVPHEPAKNGESFNDELNSWSELVSLPNILPHLIGGSTEEAQSISG
IEVATLAKVINEGNSVGVNPEVLSKSLDYDQENTVRULYIHRNVGVLTQVNDILSD
HNIEQFSHSHEIAVILMDISSVNSEIKDIEKLNQTSKVSIRLLY

>Y1R037W, 992 bp, CDS: 501-992 (SEQ ID NO 221)

GTTTTCATGCTTTTGGCGGATTTCTTCACCAACGCTTCCATTGAGACCTGTCGTA
TGTGCGAGACAGATAGACAAATTTGCTGACCGTATCTCTTCCAGAAAGAGTTCGAC
CAGCTTCGCTTCTGTCAGCGCTGAGACGATGATCTGCTTCCAGAAAGAGTTCGAC
TACCAATTTGACGAGCATCCACGGGAGGCACTGATATCAAAATTAACCTTGGCCATAT
CCCTCTTTGACAGATTAATAATTTCTCTGCTGCTGCTGCGGAGCGCTTATTTTC
CTGTAATTCCTCTCTCTCTCTGATATGCTTTTATGACCTTCCCTTGAATAAGGTCGAA
AAGTGAATAAAGAGGAAAAACATGAGAGACATGCTGCTCCCTTGAATAAAGGTCGAA
CAATGATTAATAAAGAGAGATGAGAGCTTCTCTCTCTTCCAAAGCTTCATCTC
GTAAGATTAATCAAGTTATATCTATGAGAAATTTCTATAGCTAGACCTGTTGAACAAAG
GCCAACATCCCTTCGACCAATTAAGGAAAAAGTGTGCTTATGCTTTAATGTTGCTC
CCAAATGATGATTAATCTCTCAATTAACAAAGATGAGAGCTTGAACGATTAAGG
AGAAAGGATTAATGATGAGGTTCCATGACCAAGTGTGGCCACCAAGAACTGAGCT
CTGATGAAGAAATTTGCCAGTTCTGCCAATGACATAGCGGTGACCTTCCCATTAATGA

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AAAAAATGACGTTAATGTCGACGATGAGACCTGTTTACAGTTTGTGAAGGCCAA
AATCCGTATGTTGGCTTGAGAGTATCAATGGAATTTTGAATAATTTCTATGATGA
AAAGGTTAAGTGTACGAAGAATATCTTCACTACCAACCTTCTTCTGTCGGA
CCATGCAAGAACTTTTGAAGAAGGTGAATAG

>Y1R037W, 163 aa (SEQ ID NO 222)

MSERKLAIPVDKKGQPPFDLKGKVVLIIVNVASKGFTTPQYKELEALYKRYKDEFTII
GFPCNPGHBPESDEIAGFCQUNYGVTPIMKIIDVNGNEDEVYKFLKSGKSGMLG
RGIKMNEKFLVDKKGKVERYSVLTFRPSLSLSEITIEELKEVE

>YJL161W, 1043 bp, CDS: 501-1043 (SEQ ID NO 229)

TCATTAAGTCTGGGGGATATCTTCGACAAATTTCAATATCTCCATATGATTAATCTG
TTAGCTCGTATCCACCAAGTGAACCTGTTCTTATCAATGAAGAATATGAGTCTTCTG
ATATGCTTAATCTTGCCTCATTAATTTAAATTTCTTCAATGATTAATATGATTTTGC
TTGAGCAGATGATGATGATATTTTATTAAGAACATTAACCTGCTTAATATATGATGAT
GCTTAATAATTAAGATGCAATGCAAAAGTGTATTTGCTGCTTCTGCTGCTGCTGCTGCTG
CCACATTCAGACCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TAAAACTCTCGGATTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATTAGTTAAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATGAGATCTTCAATCATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CCAACTTTTCAAGGACATGCCCAATCTTGGCTCAAAAGCTTATGATGATGATGATGATGAT
TGTCACATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATCAATATGCTTGAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACATTTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATCAAGAAAGAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTCACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTAATGAGCAATTCACCTTAAGGAAATAATCCATCTTATTAAGGAGAGTGTGTTAGTG
TTTAGGCTTCCACCGTTGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT
AAGCTGAGTGGCTTGAATGA

>YJL161W, 180 aa (SEQ ID NO 230)

MLYTRLRHNSQTFRFSGTPNLGSKPLYSKGLYSLVLTLYGTGLACLYLESNLIK
SKEDPHALIAEDDIIVADPNRIEFPALDYOKEKLDLQKSLHVLHSLVTSYSDVSQ
FSIWMFLIQLSSLIQNSTLQKRSILYKGSVSVLGRPLIYMAIKLIMQLEKAGVPE

>YJR096W, 1349 bp, CDS: 501-1349 (SEQ ID NO 233)

GATATTTCAAGAAATGACACACAAAGCCAAAGCCATTAAAGTATGATGAACAATG
GGACTACAAATGAAATTAAGAAAAATTAAGATAGCTAGAATCAATTTATTTATGCG
OCTATCTTCTCTTATACCTPACACAAATTAAGACGACATTAAGAAACAAACAAAT
GAAACAAACCAATTAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTTTTGTCTCTTATTTAGGCTCCATAAGCGGCCATTTTCCCTTACTCCCTTTTTC
GTAATATGATTAATGCTCGAAAGAAAGCAATGAAGTATGATCAATCAATTTCTGCTG
GTGATATGAGGAGGAGGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
AGCATTAAGCAATGATCTTACTTATGATTAATTAATTAATTAATTAATTAATTAATTAAT
AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TTCCAAAGATGCTTTTGGAAACCTAACGATTTCTTAAGTTTAAACCTTTTCAACGGCTTAA
ATGAAGTGTCAAGTGGGCTTACCTCATTTGATGATGATGATGATGATGATGATGATGATGAT
AGAAATGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGGAAATCTTCTTACTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
CTGCCATTCGCGCAATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TTTCAATTCGCGCAATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
CGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATGAATCTTTTGAATGTCGACAGAACTGAAGCACAAAGCAGTGTCAACAAATGAGATAT
CACTTGATTAATGAACAAGATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAAT
AAGCTTGTGCCCATTTGTGTGTCAGGCTACAAATTAATTAATTAATTAATTAATTAATTAAT
CGAAAGGTGAGACCGTAATCCAGTCAAGTTTATGATGATGATGATGATGATGATGATGATGAT

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ATTTACCACTACCGAAGACTAAAACTGTGAAGAGGTTAGAAGGTAACTTCGACGCTTACA
ACTTTGAACTGTCAAGACGAACAGATGAATAATTTCTTCATCATCTCTGATGCTTATGAGCCTA
CCGATTTGGGAATGCACAGACGCGCCCAATA

>YJR096W, 282 aa (SEQ ID NO 234)

MYPFKYKLSNGFKIPISALGTVDIPRSQTAIEIVBVGKCYRHPDPTAVLYGNEKEVGDGI
 IKWLINEDPCNHKREEIFVYTTKLWNSQNGYKRAAAIRQCLNEVSGLYDIDLLLIHSPLBEG
 SKLRLETSRMLQDAVDEGLVSGTGVSNYKGGKHIDELINWELPKHKHPVNVYETISPMWNRQ
 ELADYCKWAGLVEAPALCHGYKSNVTPDLLKVCYKVEDNRNGQVLIKWSLQHGVLPLPKT
 KTVRRLEGNLAAYNFELSDEQMKFLDHPDPAEYPTDMECTDAP

>YKL065C, 1121 bp, CDS: 501-1121 (SEQ ID NO 241)

CTGGCTAGGTTTCACATATCAAAAGAAGTTATGGCTTATGTCTCTTTCTTAAAGTTTGA
CCCTATGCGCAAAAATTTCTCGTAGATGGCGCGGTGAAGCAGAAATPATTTTAAAGT
CGGCTATAAAACCTAGATGAAAGAAGGGAGAGATAAAGCGCAGAACACCACTACT
TTAAGGGGTACGCAAACTTTGGGCTATCTATATGTATCTACTACTTCTGCAACG
TCTTTTACCTCTCGATACGTACTGTTATGCCCTGACAAATTTACATGTAAACCGGACG
TGCATGCTATATACAGGATATGTAACTAAAGGGGGCGCTACTAAACCTCTCTGGGCA
GTGCAAAATAGAAATATATGCCATGGGACCTTGTATAGTTTCTGGTTTAAAGCTGA
GTCATTGTCACGCTCTTCTGCTATCTGCAATGAGTGGCACTGTGAAACACCGA
GAAGAAATAATATTTGGATGAGTTTATCTTTACGACATTTATTTTATTTGCTCATCG
TTAAGTGGGTATATGCTCTATCTCTGTTTGGCTTTGCCATTTCCGGATCCGTAGGGGT
TTTGTAGCACAATTAACCAATTTACAGCGACGACGACAAATAAAACCTATATCTTATAA
CGGGTTGCTGTTGGCCCTGTGTTTATGTATCTATGGAAGAAAGGCTCAAAATCTGGTGT
CATTTACCAACAGCAACAGTGGCTCAATCGGGTCACTCTGCTGTAACTTCCAATACAGG
TTTCTATCTGTATCCCACTGTCATGTTGTGCAAGAGCTGTGAAATACCAAGGCT
TAATCAACGAACAGAAAGCAAAAATTGAAACAAACCTTCTCTCAACAGCAGAAAGACT
CAAAATGAAGCTGATTCACCAAACTTCAAGAGGAAGCAATATGGGAAAAAGCAAAATTTCTCGG
AGGGCTTACAAAAGCAATCTAAACTCTGGAGAAATATTTTGTATGAGAGAAATCAACCTG
GAAATGTAGCAGCTCTCTCAAGCTTCCAGAAAGGAAACTTA

>YKL065C, 206 aa (SEQ ID NO 242)

MSLYFTTFLP LLLTVEVWMLP IFVLPLPRIRRGIFSTYQNLAKQIKTIFITGCVLUGL
LFIDSWKRSQIRVSLYHNDSIGSSAVTPTQALASRANORMYISGFI LVSICPT
VMSLVKFLYKQVQGLINEQEKQKKNSSKDSNEADSTYKQEEURLKQISLUGLQKV
KNLEKFDENKONGVAAAEASKKGN

>YKL196C, 1103 bp, CDS: 501-1103 (SEQ ID NO 253)

AAAGAGGGTTCCTATTGGAGGCAATAAATAATAAAGCACCGACCCATATGAAGAATAATCCCA
TTATAAGCCCGCTGTGTTTTCTGATGGAGTCTCTACCGAATCAGGGGAGGAGCGCA
TGAGACCTCTGTGTTGGGCAATAACCCCTTTGCCACTCTGAATCAGGGCTGTGTTG
TGCAACGCAATCTTGACGACTAGTTGCGAAGCTTTGCAATAATATACACTCTTTTGA
TCGAGCCTACTTCCAGTTGGTAATTTGGTGTCCAAATTTACGATATATATGTTTTTAA
CCAAAAATTCGGCTCCTCTTTTCTTTTATTTGGGTGGCGTCGGTACAGAACGATT
GGCTTGGTGTGAATAACAAGAGCAGCAGCAATGATTAACATGAACATATACAAAGT
CTCTCGCACAGTTGATCGCTGTACAGCAGCTAGGGCAATTTCTGAAGTATACGTTCA
CTAGAAAGTTATTTTGGCAATAGAAATCTACTACATCGGTGTATTTTCGCTCTGGAGGAG
AAAAAGCTCTAGAGTAGAAGTTTAAAGACTTGTCACAAATTTGGTTTTCTTTGAAAGGT
CTAGTGTGGCCAGTTTATAGACTTTTGTGTGTAACCGGTCGCTCTTAGAATCTGGTGCAG
GACAAACAAAGTATAGCAAGAGCAACTATTTTGTACCAAGCAGTTTCCGCCAGACGTAGG
GCATATGTGGTGTGTTGATACCGCAAGAATAATCTCTGTCAAGCAGCATACACACTAT
TAAACAAATATTTGGAATGAATATTTTAGTCGCACATCTTAAGGAAGAGTGGGCAGATGTA
CTGGAGCCCAATGATGCAATGAAATGAAGCAACTAGGACACTACTATTTAGCAATATCAAG
ATCTTGTCAACAGCTGACCTATCATGAAATTTCAACAACTGGGATGACAGCAATCG
TTTTTGTCAAAACCAATGAGAAATGTTTTTCAAGAGGTGAAAGTTGGAATTTTGGTGT

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ACAAATCGGAGTCATTAAACGGCAAGTTCCTAAATGTTTATAAGCAAGCTAAAAAATCCA
ATTCGTGTTGCATCATCATGTAG

>YKL196C, 200 aa (SEQ ID NO 254)

MRYYIGVFRSGGEKALESEVKLSQGGFFERSVQGFMTTFAETVASRTGAGQRQISIE
EGNYIGHVYARSEGICGVLTIDKEYEVRPAYTILNKILDEYLVAHPEEWADVTETNDAL
KXKQJDTYISYKQDPSQADAMKVQQELDETQIVLHKTIEVQLRGEKLDNLVDKSES.IT
ASSRMFYQAKKXNSCIIIM

>YKR076W, 1613 bp, CDS: 501-1613 (SEQ ID NO 259)

TAAATAGTTGAGGCTTTTCTCGATCTCTCAAGAAGGGTATGTTATGAACTATGCAAAAT
GACACTGTAAAAATGATATCATATACCTTGATATATGGAGTGAATTTCTTCTCTTTTATTTT
ACATTTAGTTTCAATATATATAGGCAATATAGGGTATAGTTTAACTATTGA
TTATAAAAGTGTACAGAAAGAACCGACCAAAAGCTTGTGACGCAAACTTTTCCATC
TTTATTTCCACCTTTCAGAGGCTCTAAGACCTTTTGAAGTATCAATATAGTTTATCA
TCTTTTCTTGTGTGTGCTCGTTACTTAAGTATAGTCTCTTGAAATTTTCAACCCC
TCATTTTGTGTTTGGCGTCCACCCCTTCAACTCTAAGCTTTTCTGTTATTAAGGTA
GTTAAATTAGGTAACGCTGCTTTTACCCTACATCACTAGTGTCTACGAGAAATTTACCCAAACC
CTGCGCAAGATAATAAGAAATGTCGAACACAGTGGCGGAGTGTATCAAAACGGAGCTTTCA
CAACAGGTTTCTGCTTTCATAGAAATCAATCTTAAAGCAACCAATATTAAGCGAG
AAAAGGGAAGATATATGGTTTATGTTATCTTCAAGTCCCATGGGCCCATATAGAACCTAA
TTACGAGGCTTTGAAGGGATTAACCTCTGTTATAGGATGTAGCTAGTGTCCATTTGGCACT
TTGACAGGAAGGATGAGGATTTTTTGGACATCGMAAAGCAATTTGGAGGACAGTGAAGATT
TTTTGGAACTATGGCAGCATGTTTGCAGGTGTTATAGAACTGCTTAAAGGAGTTCTTCAAG
AGACTTTCGGCGAGCAATCAAGATATGACATGAAGATTGATTAAGTCTTAAAGGAGTTCTTCAAGC
CTCAATATGGATACAGAAGAAATCAGTGACTTATATTAAGAAGCGATCTCTCAATACTCGG
CAAGGTTTCAACCGTCCAGTCTGTGGGACTTAAAGCCCAACAAATTTGTTTAAACAACGAA
TAGCGGAAATTAATAGGATTTTGGAACTCTAGTGTGCTTCAAGTAAATTTGTTCGACGAGCAT
ACAGAAGAAATTCAGGCTTTCTGCTCTTGTGMAAAGCAGATGATGATCTCAATTTCTT
GGGTTTACGACAGCATCAACAAATGGTGTATACAGAACCGGATTCGACAGAGAAAGCAGAG
GTTACAGAAAGTGAAGTCAACACGTATTTGAACATTTTGAACAAGTGGACAGAAATCTCTGA
GTGACAAATTTCTCAAAATGAAGGCCAAATACGGTGAAGAAGATGAAGAAATCTTTGG
GTGAGTTTCTTCACTGTGGGTGATTAATTAACAGAGCTGACATATAGATTTACTACTACG
TCATAGAATTCGATCTGTGTAGCTTCAACATTTTCAATATGCAATTTTACTCTTATAGAG
CGGGATATCAATTTTCAATTTTGGGTGAAGAAATTTTACTTGGAAATATGATGCTTCA
GTACACAAACAGATTTTTCAGACCATATCAAGTATGAACTACTACGGGTCTCCACACAGGATCA
ACCTTTGGGAATTAACGCCCTTGGAGCCCAAGCCAGATATTCGTCTCTTTTAA

>YKR076W, 370 aa (SEO ID NO 260)

MSQWASGTFNGAFKQVUSSFRETISKQHPYKPAKGRWYLVYSLACPWAHRTILTRALKKG
LTSRIGCVVHMLDHKGWRLDMEKQLDESDFLHWHVDVAGGITAKEDSSKSPAEIK
NDQSFVGNEDHEGYKRLSDLYKSDQPSYASRPTVPVLDLETQTVINSSSEIIRI
LNSAFDEFVDDHKKHTLDVPAQLTKTDJDNFSNVYTNNGVYKTFPAEKAEVYSEVN
NVPEHLDKVEKILSDYSKLKAKYGEEDRQKLGFEFFVGDQLTADIRLYTWTYVIRDPV
YVQHKCNFTSIRAGYPFIHLWVRNLWYNYDAFRYTFDTHDKLHYTRSHTRINPLGITT
LGPKDPRL

>YKR092C, 1721 bp, CDS: 501-1721 (SEQ ID NO 261)

[illegible]

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AGGTAAACAAGCCTTTTCAATATCTTGACAAATTTGGAAATCTTCTTGGAACAAGAAGTACA
CAGATTTTGGAGCGGAGTATGTGAAGACAACAAGGACAAGATACTAGATCGCTACTTTG
CCATCGGAGACATCTGACCGAGGCGAGCTGAGACTCTATCCCAACGATGATGAAGTTGG
ACGTGGTATACCATCAACACTTCAATGCAATCTGGCCACCATCAGAGATGATTAATCC
GTATACACACGTGGCTCAAGAAATATATCTGGCGCCAGGAAGCTTCCAGCGCAACAGG
ACTTTACCCACATAAATCTGGATATCTGCTCGCAGCCAGCGGTCAACCCGATTTGGGA
TCACCCCACTGGGCCCAAGCGTGATATCCGACCTCCATGA

>YMR251W, 366 aa (SEQ ID NO 316)

MSEKASNNKAEPKQSPPREIISADHPYKPAKGRWLYVALPCPWQRILTILRALKG
LAPITIGSVAHWHLDDKGRFLIEEGDKNERHWFDIAGGISVNLANTSTPVANPNNAH
RLVVDGDEPHVGYKRLSDFYFKTKDYKGRFTVPVLWDLCTIVNNESDIIIGMNSA
APDEFVGEYRQVRLVPSLEAQITFNSWVYDKINNGVYKAGFAECAVEYREVTSLFQ
YLDKLENLDDKYITDLEAEYKNNKKILDRYFAIGDTLHEADVRLYPTIVRPDVVYHQH
FKNLATIRDDYSRIHTMLKNIYWRHEAFQRUTDFTHIKLGYTRSQPRVNPITPLGPK
PDIRPP

>YMR273C, 3248 bp, CDS: 501-3248 (SEQ ID NO 321)

AAATTTGCTCAATCTGGAATAGTCTACTTCGCACCTGCTGCTGCTGGATTAATATCC
CTGAAGGATACCTTCAAACTCTGTGAGGAACTCTCTGGTTATAGATAACCTTTTAGCCT
TTTTTACGATCTTATACCTTTTAAATTTCTCTATGCTATATACATTAATACCTTTCTACT
ATTATGGAATCTTATCGACCGCAGCGGCTTTTGTACGGAAGAGTGAATAAATCTAGCTT
TGGTTTGTGGAAGAATTTGGAGACATATAAGTACCTATATCTTTGTATACGGACT
CAATAACAAGCTGCTGCTAGTGGTATGAAGTTGTCAGATCTAAGAGTAGAGAGAAG
GTGCATCTAATAGTGTTCGACGCTTTCTCTTTTAAAGGTTTATTTTGGTCTCTTAGA
ATTTAAGCTCTTAGTATAGTTGCTTTGTTTGTGGTTCATATTTTCAATTCAGAGA
GAAATTTAGCTTTTATTAATGCTCAATAGAGATAACGAGAGATGCTGCTGATCTACAT
CAAGCGATAAGCGGATCGCTGATCAAGGATAAACCGAAGCTGGAAGTTTGTATGCTG
CAGACTCTTACATAGAAATCCGACGCTATAAAACCTAAAGATTTGTCGATGGGT
CAATGGATTCTATTATGATCGAATAGATATAAATTTCTGGTGGGAATCTAGTGGT
GAGCATATGCTTGCACGACATCACTCAGTTTCTGCTCAATGCCAAGTACCAACACCG
TTAATAACACAGATATAGGATCCAACTCCGCTAGAGAACTTGCATGGGAGGGTAACT
CAGGGATAGAAATCTTCAATAGATATAACAGAGTAACTTCTTAGGTATATAAAGGTTG
TTCACTTCCATCCAGGAATTAATGCTAACGTTAATGAAGAAACCTTATTTATGGTTT
CCGCCAATAACACCCCTAACGTTTAAGCTGATATATTCCTAGAGCTTGTACAGATACTT
TACAAATATACAACTAAGCGACATGGTGAAGATAATGATGGGAATAGCAATGAATAA
ACGATATTGAGGATTAATGGGAGGATAAAGAAATCACAATCATATGAATAAAGGAGA
ACACTATCACTTGAACAGGGGCTGTCAAGGCATGGNAACCGCTCACTAATACGAGGC
GAGACAGTCCCTGCAACAGTAAATAAAGTCGAAGAAAGATCTCCAAATAAAGAGA
GACGAGTCTGCTTAAGAGATATAAATCAAGAACTGACAAAGATCTCAATAGTGCAGGAC
TAACCGACAATGATGCCATTACTATTAGCCAGAACTCTTAGTATGGCTGGTTTCATATCAG
ATAAAAGAATCAACACACCGAAGGCAATATGATGAAGGAGATATGGTTTTCATA
CTTCAAGCGCATACTTTGGATGATGGTGAAATTTGCTCCAAATATGCCATCAATAATA
CCATGACATGGCTGAACGATCTCACTAGAGAGGAGTAGATTCAACATTAATCGAATCA
GGTCAACAGACGCAAGAAAGAAGTAGAGACAAGTGTGGATGAATGAAGAACGACGACG
AAGAACGCTTAAATTTGACCAAGAATACATAAAGGTCGCAAAATAGCTCCGACAAATCC
CTTTTAGACGCAAGTAGGATTCTGAGATATAGTTCGCTGGGTCAATTTGGTGATT
TTCAAGACATTTATATCAATACAGACAGTCTAGTGGCGAGTGGGAACAAGAAATGGGA
TAGAAGAAAGACCGAAGAGGTACCGCTCAAGGTTGCGAATGACACACTAGAACAAAGCT
TAGAGTTAAGAGAGGGAACAACAGATAGTTAAGCCAGCGCAACGATGACAAAG
AAACGAAGCGCATCTGTCGAGAAACCGATGGACATGGTTGCAACATTAATGACGAGAG
AAGACGATTAACGAGAAACCAAGGAGGACGATGAATAAGAAAGGATGGATTTCACAA
GAATGGCTCGACATTTCCAAATAACATTTATTTCTCTATTATATGCGGTGAGAAGA
CGAGGAGTCTCAATTAAGAGAAATGAACAAATTCAGTACTTCCACGCGACATACAGA
CAAGACAGAAATCGAGAAAACTTTTTCGGAACCTATTTCAGAGAAAGCCACCAACAGC

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ATGATGCAATCATCATCACCCTCTGCTGCATCATCTGTCACCATCAATACCAAAATAACG
ATGCCGTGCAGCTTCCGTGAGGAAAGCAAAAGCTTTGGTAACAAGAGTGAAGGAGGAGC
CGTTGAACCCATTTGTTGGCAATCGCCTCTGCTCTCACCGTCCACCATCACAGCCGTC
ATGTTTCCCAAAAAATAAGGTAAACCCCTTAAAGATTCTCAGCCGACGACGACAGATAC
CATTAACAACCAATTTGAAGGCGCAATAGAGATAGAAAGAAGAAGAGGAAGGATTTCG
AGCTTTGCCCAACTACAGCTACGCGCGCTTAGTTAAGTAGTACCAAAAGTAACTCTTAGAG
ACAGAGAAGAAGAGGAGGCAAGAAAAAGAAACAAGAAGAGAGGACAAATACGACAGAAATTT
CAACCAACAACACTCTCAACACGTCACAAAGGAGAAATACCGATGAGCAAAAAGCTCAAC
TACAAGTCCAGCTCAAGAAACAAGTCTCAAGTCCAGTCCCAAGCTTCAGCCCCAG
TCCAAAAATTCAGCCCCAGTCCAAACTTTCAGCCCCAGTTGAAGCTTCAAGCTCAAACTCAG
CTTCAGCGCACACCATTTGAACATACCTCATATATGCCCCCAAGAAAGCTTACATTTG
CAGACGTCAAAAACCTGACAAACCAACTCCCGGTTCAANTTCACAGACAGTGCCTTTG
GGTCCCTACCTGCTGCTGACAGTCTAGCGTTATCATGTTTGACCCACCGCTTACCAA
TTAAGCTCAAAAGGGGCATATACCGCTGACTCACTTGAATTTGAGCAATTCGAAGAGGG
GACTCGCGAGCAGGTTATTATAGTTAACTTATGTTATGCTTATCTGAACTTGGTTTAATC
ACACTCTGTACATGAGGAGGTAGCCCAACGACAAAGAACAACAACAACAACAACAAC
AACCCCTGA

>YMR273C, 915 aa (SEQ ID NO 322)

MSNRNESHMLRTTSSDKAIASQRDKRKSEVLIAAQLDNEIRSVKNLKRISIGSMDLID
PELDTKFGESGSRWSGTTSSASMPDPTTVNNTRYSDPTPLENLHGRNGSGLESSN
KTKQNGYLKIGVHSPSRKLNANVLKNLLWPNQHPNVKPDNPLELVQDTLQNLQS
DNGEDNGNSNENDIDNGEDKESQSYENKENTINLRGLSRHGNASLIRPSTLRRS
YTEFDNEDDDNKGDSEATSVNKEVERISIKERPVSLRDIETBELTKISNSAGLTONDAI
TLARTLSWAGTSDDKXQPOPEGHYDEGDTGFSTQANTLDDGEFASNNPNNNTWMPER
SSLSRSRTYAIRSQEKEVEQSDVMKNDDEERLKLTKNTIKVEIDPHKSPFRQDE
DSENNSSPGSIGDFQIDYHNRQSSGEWQEMZIEKEAEVYKVRNDTVQDELEIREGT
TDMVKPSATDDNKETKRHRERNGTWLNKNKSRDDNEENQDDEENVDVSQRMELDNS
KKHYTSLFNPGSTEYENKEMNSSTSTATSTQRTKIEKTFANLPRRPHKHDXSSSP
SSSPSSPSIPNNDAVHVVRVKRKLGNKSGREPVEPIVLRNRPFRPHRHHSHRSGSKIS
VKTLKDSQPQQIPLQPLEGAEIEIEKKESDSLSLQLPQPAVSVSSTKSNRDRBEEA
KKKNKRSTNTETSNQHSKHVQKENTDEOKAOLQAPAOEQVOTSPVPQASAPVQNSAPV
QTSAPVEASAQTQAPAAPLPIKHTSILPPRLKTPADVKPKDPKNSPVQFTDSAFGFLPLLL
TVSTVIMFDHRLPINVERAITYRLSHLKLNSKRLGQVLLSNFMVAYLNLVNHLLVMEQ
VAHDKBQ000000000

>YML112W, 3143 bp, exon1: 501-1773, intron1: 1774-2775, exon2: 2776-3143 (SEQ ID NO 327)

CTTGATGGATTTATGTGACGTTGTAGAATCTAAGTTTACTGAAAAAATCAAGAGCATGTA
GATGTTACGGATCGACTCAAGACCCCTCTGCTACTCTGAAAATTTCTAATAATTATGTCACA
CCACCTAGTATAGATACAGCTTGTATTTGTATCCGCTTTTATAGTCGTGCTATTTTAAAA
TCTATGATATAATACAGATATAAATACACCTTCGTGTACAAAGTGTCTAATAATATGTAG
AATTCGAAATCTCTTTTAAAGCGGTATTCGTATGTAAATGATGAAATAATTTATTTCTT
TTTTTATTTCTTTTTTTTTTTTTTTTTTTTTTTTTTACGCCGATCTCATCGCAGAAAT
TTTTCTCTCATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT
TTCTGTATCTGATTTAATTTATTTCTGTCACACCTGTAAACAGATTAAGCAATTAAGCACT
AAGGCAATTTAGAGCAATATGATTTACGTTGGTAGAGATCAGCAATATAACAGACTA
ACTACAGCTTAGAGTGGCGACTTCGCGGTGGAAGAACTCTGATAGAAAATCTTTTACA
ATGACAGCACCAAGCGGTAACTACCGTGTGTGTTCCGTCCTCTTCCCAATTTTACAAC
AACCCAGGAAATTTGATCAAAACCAACTGGGATGAAGAAATTAACCAAAATTTGCCAATTCG
AAAAGAATTTCTATTTGAACACGAAAGTGTTCGCGACAGATCGGACAGTGAATTTGCTC
AGTTTCAGAAAGGAAATGAATGACTATTTCCGACACAGATATTTCCAAAGCCCAATCACA
CTTTTCGATGAAGCTGTTTCCGACTACGTTTTCGACACAGATATTTCCAAAGCCCAATCACA
ACAAACCACTGCAATCAATGTCAGGCTTGGCCAAATGGCTTTATCTGTTAGGAGCATG
TTGGTATTTGCTGCCACTGGTTCCGTTAAGACTTTTGTCTTATTTGTTTACAGGATTTGTT
ATATCAAGCTCAACCAATTTATGCTCCAGCGATGACCAATTTGTTTGTGTTTGGCTC

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CAACTAGAGAAATTCGGCTGTTCAAAATTCAGACAGATGTTCCAAAGTTTGCTCATAGTTCCA
GAATAGAGAAATACCTGTGTCTACGGGTGTGTTCCAAAAGATCAAAATTCAGAGATTTATG
CTCGGCGCTGGAATATGTTATGTTCTACTCCAGGTCCGACTAAATGATATGTAAGATTTG
GTAGAGCTTAATTTGGAAGAGAGTCACTTACCTGGTTCTGATGAGAGCTGATTAAGATTTAG
AATAGGGTTTAAAGACCAATCAGAAAGATGTTGATCAAAATCAGACTGATTAAGACAAA
CCTTGAATGAGTCTGCCACTTGGCCAAAGAGGTGAGCACTAGCGCTGATTAATCTTGA
AGATCCCAATCAAGTTCAAGTGTGTTCTAGAACTATCTGCTCCCAATATTAATCTAC
AGATGCTCGAAGTTGTTCTGATTTCCGAAAAGAGATGTTGTAACAGTACTTATGAAA
CAGCTCTCAAGACAGAAATCAGACATTAATCTTCTCTTACGAAAAGAAATGTGGC
ATGATATCAACCAAGTATCTAAGAGAGATGAGATGAGCCGCTGCTATGCAATTTGATCA
AAGACCAAGAGACGTCGACTGGTGTCTACAGAGTTTGAAACGCTGATGCCAATTTTTT
TGGTGTCTACTGATGAGTGGCCCGCAGAGGTATCGGATGTTAAATTTCTCCACTTTTTT
ATGATATTTTATTTTGTGTTTACCTTACGATTAACGATTAATCAGCTATTTCCAAATGGCTTT
AATGACATTAATGACTTTATGACAAACATGATAGTACAGAGAGACACCTTTTTCCTTTT
TTTTTTTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
TCGAATCTAGACTCTATGAGTCTATTCGATGGGAGTATCGAAATTTGAAATTTTAA
TTGGAATGACTCTATGATCATCATACAGAAAATTAATTTGGAGAGATGAGAAAATTTG
ACTTTAAATTAAGTCTTTTGAAGAGAGGAAATTAATACTGGGAGTGTATTTGTTGTT
CATATTTGCACTTCTCATCAAAAAGAAATTTGCTTTTGAACATGGCGGCAAAATTAACAA
GAAATTTGGCTTTGAGCTTAATTTCTAGAACGCTACATACGCTTGTGATCTGTGTTT
TTTCAATGCTTTGGAGTTTGTACAAAGGTATGTTTATTTGAAAATTAATTAATGATTAAT
CTACTTTGAAATTCGCGTCACTTCTGATCTATGATTTCTCAATTTTGAATTAAGAGTGTG
CATTTTGTGTAATTAATGAGATCTGTGATCCCAAGTTCGATTTTGAATTAAGATTTACTTT
ATTAATAATGAAATTAACAAATTAATAAGAGATTTCCACCATTAATTAAGATTTACTTT
GTTTCTCTTTTCTTTTAACTGTAGCTTTTCAATTCGATTTGAATTAAGATTTCTGAGATTA
TGATTAATTAATTTGAAATTTCTTAATAATAATTAATTTCTGATTAATTTCAAGCAGAGG
GGAATTTGAGACAAATGTTGGAGTCCAAACATGATTTTGGGGGAGATGAATAATTAAG
TTCAATTAACAGATTAAGACCAATTAATTAATTAATTAATTTGTTGTTAACTTTGTTTCT
TCTTAATTTTTCAGATGTTCAAAAGTATCAATTAATTAATTAATTAATTTCTGATTAATTA
ACATTTGAAGATTTGTTCAACAGATTCGTGAGACTGTGAGACAGTCTACTGTGATCACTG
CTATATCTTTCTTCAACCGAACAACAAAGGTTAAGGCTAAATTAATTTCTGATTAATTA
GAGATGCTTTATCAAAATTAATTTCTCCCAATTAATTAATTAATTAATTAATTAATTAATTA
GCGGTACCCCAAGATTAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTTACGGGTGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
ACAGAGGTCTTCAACTATTTGA

>YNL112W, 546 aa (SEQ ID NO 328)

MYGGDDQYKNTKMYKSGDFRGRNSDNRSTADRPQGANVYRGGRSHSNYNQPOELIK
PWWDELPLPTPEKNTYVEHESVDRSDSEIAOPRKEMEMTISGHDIKPTTDEBAGF
PBYVINEVNAEGFDKPTGIGQGWPMALSGRDMVIAATGSGKTLSCYLGIVHINAOP
LAPGDPPIVULAPTRELAVOIOETESKFGHSRLRMTCVGGVPSQOIRJLSRSEIV
IATPGLIDMLEEJGKMLKRVYLVLEADNRLLDMGFEPQIRKIVQIIPDRQTLIMSAT
WKEVQOLADYLDNDPIQOVGSELSASHNTQIVLEVSDPEKRLAKLYLETASODNE
YKTLIFASTKRMCDITKYLRLEDGWPALAIHGDQOREDMVLOEPRNGSPIMVADIVA
ANGIDKGVINVINVDMEGNIEDYVHIGRTIRAGATGTALISTFTDQNKGLAKLISIMR
EANQNTPELLKTYDRSTYGGHPRYGGGRGGRGYRGGYGGGRGYGGRNQJRDGWMN
RGHSNY

>YNL131W, 959 bp, CDS: 501-959 (SEQ ID NO 329)

CAAAAAGAGCTAATCACTCTTGAACCTAATTAATACGCATTAATGATTAACAGTGAAG
GAATGGCTGAATCTCAAAAATCTTGAATAATGCTGCCAAGGCCAAAGCGTGTGACAT
TTAAAACTGTGTTAAAAAGAGAGACTGAAGAGCTGAAGATTAATCTATAGCAAGAGATG
AAAGCTATGAAAAAACCAGAAAGTCTAAAAAGGCTGCAATTAATTAAGCTTCTACTTTG
TCAAACTCTTTTATAGCTTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AGTTGATGTTGAACCTTTTCAATATTTCTTTCAATGCTGTGAGAGATTAATTAATTAATG
ATTATGCCGGGAAAACTGAACCCGTTTGAACAATTTCAATCAACATCACTCCCTCGT

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AGTGAATTAATCTTTTGAAGTAAATACGAAGTAAACCAAGAGGTCAAAAAGCACTAATTAAC
CCAAAATAGCAATCAATTCMAATGTCGAATTAATCAATTAATTAAGAGAGTGTGCTCAAT
TAGAGAAACCAATATTTCCAGAAATCAGGCCATCTGTGAAGAAAGGCTTCTCAACAA
ACAAAGAGCTTCTCAATGATGAAGATGACTGTATAGTGAATTTGAAAGATTAATTTGATG
AAATGAACATTTGTTGAGACAGATTCGTGCTTTAAAGACATGTCCTCCAGGTGAAGA
GACAACCAATTTCTAATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT
AATCCGGAACCTTGTGAGACTTGAACACACGCTGTTGTTGATGACGTTGTGTTGACAT
CCTTATCTTACTTGGCAACACACCTTAATCGAAATGGAAGATGCTGACCAACGCCAATTA
GTGATGCTAATTAACATTTGGCCCAAGGTGAAGAAAGATGCTGACCAACGCCAATTA

>YNL131W, 152 aa (SEQ ID NO 330)

WELTEIKDIDVQLEDPQFSRNOIYEEKASATMNDVDEDDSDSDPEDEDENETLID
RIVALKDIDYIPGKRQNTISNPFQSTSFVRNAPFTSGNLAWTLTTTALLGLVPLSLIAE
QOLIEMEKTFDLOSDANNITLAGEKDAATN

>YNL143C, 893 bp, CDS: 501-893 (SEQ ID NO 333)

GAAATTAACACAGCGGAGAGCAATCATGAGAGCCCAAGCAAGATTAAGACATGCTTTT
CTGGATTAACAGCAATTAATTAATTAACGATTAATCTGGGACATTAATCCACACCTGTA
AGCCACAGCATCAATCCATGAGGCAAGTCAATATGTTGATTCAAATCTGTTGTCA
CGAGTACCAACCGCTTCTTCCGCTGTAGGCTGACCTGTAATTAATTTGTTCAAACTCT
TATTTGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
GTGACAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TACTACCCAGTATGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AGGAGCTGCGAATTAACACCTTGTGATGATGATGATGATGATGATGATGATGATGATGATG
ACGCGCTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AATTTACATTTCTTATCTTATCTGCTTGTGATGATGATGATGATGATGATGATGATGATG
ACAGCACTAAGAGAGAGCGGAAGATCTTCTTCTTGTGTTTACGAAATTAATTAATTAATTA
AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
CTTTCTTATTTGAGAGCGCGGATTTGCAAAAGGAAATTAATTAATTAATTAATTAATTAAT
TGTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
TTTCCAAAGAACGAACTTAAACCGTCTGAGAGCGGCGGTTAATCGTGA

>YNL143C, 130 aa (SEQ ID NO 334)

MRBDLKLFTRELVDFTPLISGFDYQTLIISNSKKRPXDSLSSEKKKKKKKKXDV
LSYSLYLDLPFVPLFMQPGYSQREKPRQHSLEFIMTLTKPMISWADMYVVSKNLSL
NRPAEREGNR

>YNL19C, 938 bp, CDS: 501-938 (SEQ ID NO 335)

ACAGCGTTAATTTCAAAATACCTTAATCGAGGCTTATCTTATTTTCAAGGCAAGC
TCTCCACATCGGTAAGTATGACCAATTAATTAAGTGTGCAAAAGTGTGTTGTTTC
ATACAGCGCCGAGAAACAGATGATGAATAATTAAGTGTGCAAAAGTGTGTTGTTTC
CCGAGCGCCGCGCTTCTCTCCCTGAAATCTTTGTTGTTCCGCCCCCTCTCAATA
CCGATCTGCACTTATCTTACAGTCAAGTGAAGTGAACCGGAAATTAATCTCTGCTGT
TTGCTTGGCTGTGAGCTTTTACTTGGGTATGCGAAGACCTTGAAGAGTTGAACCGGCT
TCCTCCCTTAAAAAGAAATTAATTAAGGTTATTATCTGAGCTTAAGCAATTAATTAATTA
CGTTTCGCGGCTCGCTCAAAATTTTCAATTAAGGCTCTATGACAGACGTTAAGCA
GTTATGACGAATACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
GTGCTTACTTGAATTAATCTTCTCTTTTATTTCTTGAATTAATCTCTCTTCTCTCTATC
TTAGTCTTGGAGTACTGCAATCATGTTTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT
TTTTTTTTTTTTTACTTTTCAATTTCTGATTTCTGAGCTTTTCCATTTTGTGATTAAGTAA
GTTTAAATTAATGATCCCTACAAACAGTACGCGATCCACCAAGCAACAAAGCAGAT
CTTGAACCATCAATGATTAATCAAAAGGTTGGAATTAATCACTTTTCTTTTCTGCTAT
TGCACAGACAAATATCCAGAAATATCAATGATGATGAAATTAACAGACAGGTGGCACCA
CAAGCACAGCGCGAAATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

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>YNL179C, 145 aa (SEQ ID NO 336)

MSNCRLLCRQLSSAYNLVFPFLIYRPFSLYSSCEYWSQCFSPFFLEFLFFRFFPTF
QFLVAFPIILLFKVLSLNTKHKVRPIQRHTKARSLTHHCIPKRMNIHFPPFSGLLHKTISR
IPSWIGNTRQVAPTKHTPKYLLNTWI

>YOL150C, 812 bp, CDS: 501-812 (SEQ ID NO 349)

TTCCCAATTCCCACTGCTATTCTCTGCTATTGTGACGAACCAATGTTTACTTGAATGTTA
TTATACCAANTTTGTGATCAAAATATCTACTTCTTGTGGGAGACGGTAGAAGATTT
GTATTTGGGAGACGCTCTCAAAATATATGGCAAAACACCTTGATATTTCTAGTTTATTC
CATTCGCTCTCTTGAGTCCCATTTATACGTACAGTGTGGTGTGTGAAAAGTAGT
TGTATTTCTTTGGATGTATCTCCCAATAACGTTGAAATCAAAAGCTTTTCTATAGAA
TCTAACTGTGGCAGAGTTTCTGCTGCAGTGTGCTCGCTCATTTGTGCAAGCTTT
TCTGTGATGTGTGTGCAAGATAATGCTTATCTGAAGCTTTCTCTATTTGTTTTCGTC
AAATTTCTTTCTTTCTGCTTCCGTTTTCGACATATTAACTGTATATAGAGAGAAA
AATGGCAGAGATGTACTAGATGATAAAAAATAATTGTAATAACGTTAATATATAAAT
ATTATCTATTTTCATTTAAAGTTTATTTCTGCCCTCAAAATTTTAAATTTGGGAGCAG
TCTCGCAATGTGTCCTTTCAAGTTCTGAACTTGAACCTTAACAAATTTCTACTCTTTT
TATATCAAGAGTAGCAACCAAGGCTTTATGGGTAGCACCAGAACCTGGTTTCCCCACTG
GAATATGCTCTTTAGAACACAGGAAGTCTCGTTAAGGATATCGAGAACATCTCGCATAG
TAAATCTGGCCTCCGATACGATTAGTCTTTGA

>YOL150C, 103 aa (SEQ ID NO 350)

MTKNNNVNIYKYLPFSFYILPSNFKIWEAVSSMVSFKFLNLKPNPNFLFLLSRVAP
RVLWVAPEFGFTGILPFRGKSLRISRTSCIVNLASDTISL

>YOL151W, 1529 bp, CDS: 501-1529 (SEQ ID NO 351)

GGGTGAACATGATCATATTTCGGATTTTGGGTACATAATAATATATCATATTATTAATTAT
GTTTGCATGTAGGTTCTACAAATACATTTGTGTACGCTATAGTTTCTTTCAAACCTAGA
AAGAATTCTGTAAACAAATAATCTCCAATTTTATAGCACTTATTAATATCAATGCTGC
AATACCTCTTATTTCAACAAATTTGGCCCTACCCTCTTTTGTACAAAAAGCTGCCATTC
ATAAAAATAGTAAGAAGCATATTTGGAATGCTCAATTACGATTAAGTAAAGAAAAAATCATG
TGTACATATTACGTAAATAGAAATACGGAATTTTCTCGCGAAGTAGATCTTTCCTGGGAAA
AAAGGAAAAGATCCGATCAATATTGAAAGGGGATCCTTAGTTTCCCACTATATAAGGA
GGAATAAGCTATCTCTAGCGTTGATATACGTGTACGATTTCCTCAACACAGATAGC
ATGTCACACCGCCGTAATATGATGATGTTTTCAGGTGCTAAGCTTACCGGTTCAATTGCC
AACACATGTGATCTCTGTTGAAGGAAGACTAATAGGTCAATCGGTTCTGCCAGAAGTC
AAGAAAAGGCCGAGAAATTAACGGAGGCTTTGGTAAACAACCCAAAATTCCTCCATGGAA
TTGTCCAGACATATCTAAGCTGAGCGCATTTGACCATGTTTCCAAAGCACGGCAAGG
ATATCAAGATAGTTCTACATACGGCTCTCCATTCTGCTTTGATATCACTGACATGAAC
CGCATTTTAAATTCCTGTGTAACGGTGTAAAGGAATTCCTCACTCAATTAATAAT
TGGCAAAAGAAAAGGATAGCTTTTAAACATTTAACGAAGATCTTGAAGGTTTCTGTA
GGGAGATGTCCAAAGTACCCAGTACGCTACTGTGTTTAAAGAGTTTCTGCTGAAA
AAGACGCTGGGAAATTTCTAGAGGAATAGAGACTCTGTAAATTTGCAATTAATCTGCCG
TTAACCCAGTTTACGTTTGTGCGCAAAATGTTTGACAAAGATACAGGAGTTTCTGCTTCC
ACACATTTGCGGAACCTGTCACAGCTTGTATGCAATTTATCACAGGACAAAGATACCGG
ACATATTTGGGTAGATACATGATGTTGCGAAGGCTCAATTTAGTTGCTTCC
AAAAAGGGAACAAATTTGGTCAAGACTAATCGTATCGGAGGCCAGATTTACTATGACG
ATGTTCTCGATATCTTAAACGAAGACTTCCCTGTTCTTAAAGGCAATTAATTCAGTGGGA
AACCAAGTCTGGTGCATCCCATACACCTTGGTCTACTCTTGATATAAATAAGAGTA
ACGAATTTGTAGGTTTCAAGTTTACGGAATTTGAAGAGACCATTTGACGACACTGCTCC
AAATTTTAAATTTGAGGGCCAGAAATATA

>YOL151W, 342 aa (SEQ ID NO 352)

MSVFVSGANGFIAQHIVDLLLKEDYKVGARSQKAEKLENTAFGNPNKFSMEVVPDLSK
LDAFDHVQKHGDKIKIVLHTASPPCFDITDSERDLILIPAVNGVKGLHLSIKKYAADSV

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RVLVTSYAAVFDMAKENDKSLTFNEESWNPATWESQSDPVNAYCGSKKFAEKAWEFL
ENRDSVKFELTAVNPVYVFGPQMFQDKDKHKLNTSCELVNSLHLSPEDKIPELFGGYI
DVRDVAKHLVAFQKRRETIQRLIVSEARFTMQDVLDTINEDFPVLKGNIPVKGKPSGAT
HNTLGATLNDNKKSKLLGPKFRNLKETIDDTASQILKPEGRI

>YOR131C, 1157 bp, CDS: 501-1157 (SEQ ID NO 359)

TCCTGAACGGAAGCTGCAGTTTGTCTAGTACTACACGCTCTCTGACATAGAAATGAT
CCATCTGTCTTGTCTGAGCAGGTTTCAGAAATCTCTCTCTGGGGCTCAGCAAAATGGATTG
TTATCCAGATCTCATATAGGATTAAGGTACAGCCGAAGTCACTTGTTCAGAGAGATAGT
GGATTCAGCTAAGGTTACGTACGGCAAAAAAATAATAGATCAGCTTTTCCAAAACAACTA
TTTTGGCGTTTACCAAAACCAAAACAGATATATCAACTAGTTCAATCATCTCTTGAAGAACG
TCCCTTCTTACAAAATTAGCTTTTGAACGGTGTCTATGGAAGAAAGTGTAAAGAAAACG
AAAAAGCAAGAAAGTCAATATATCTTATAACGAAATATACAGGTTCATAGTACATCG
CCAGGTCCGCTAACACAATCATTAGGATAGTGGGCAATATATACGGTTCTCAATAGTCAC
TGAAGTGTATCACAGAAATGAACAAGCTCAAGGACTACAGGATTTAAACACATCA
AAGCGTTGTATTTGATATGCAATGCGACATTTAGCTTACCCAGCCTTGGATCTTTCCAG
CAATGAGAAACCGCATAGGAATTTGAGGACAAATCGATTGATATCTTCTTCAATTGATTA
CATTTGCCCAACGAAAGAAAAAGAGAGCGCATAGTAGAATAGAAATTAGTTGAGGCAA
AAGCCATGAAGGAGATGCAACCGCAGCTGTCTGTGTTGACATAATAGAGTATTTGACGA
AAAAATGTTATAGCAAGACATATGTACTAGAAATGTCGAGGCCCGGTAGAGACTTTTGT
TTAAAGATTTTATTCATCCGAGCTTTGAGGTTTGAATCTATATTTGACAAAGGAGTTTA
GGCTTACAAAACCGCAACCAACCCATTTAGTTTACATACATCGCTCGAAGCTTAAATATAAGGC
CCTTGGAAATGATCATGTAGGAGATTCATTTGACGACATGAATAATCCGGTAGATCTCTGT
GATGTTTCAAGTATTTACTCAAGAAATCATGTGAATGACATTTTACTGCTCGAACATTAAG
AACTAGTAGACGTTTTCAGTAGAGGATCTTTCCGAAATAATTCGAATTTGATTTCAAAATATGA
ATAAGCAAGATTTCTTCA

>YOR131C, 218 aa (SEQ ID NO 360)

MYKLQDRIELGHLKHAIVFDMDDTLCLPQWMPFAPMRNAIGLEBKSIDILHIFIDLTPKE
KKEAHLGIELVEAKANKEMOQPQGLVDIMRVLTKNGISKNICTRNVGAPVETFKRFIPS
ELSRFDYIVTREFRPTKQPQDPLHLHASKLNIIRPLEMINMGVDSFDDMKSGRSACCTFVLL
KNHVNGHLLLEHKLVDVSDVSEDLSEIIEIILQNMKNESF

>YOR286W, 950 bp, CDS: 501-950 (SEQ ID NO 367)

CATCTGAGTACTCGATTGTTCATATCTCTGCTTCCATCAATGTCCTCATATAGATCGCAC
CTGACCCATTTTGCCTTAGATCTCTTAGAATTTTGAGAAACAGATTTGGCATCCCAAAACCTG
ACAGTCCCAAGGAGCTAATATTTTATTTGTGCTCTTGGCAAAACGGGGGAGAACTCAAA
AAGTCGCTCTCCACATGGAATTAATCAACACCTCACTATATCTCTGCTCTATATGAATGATT
GGGTTTCTCATGGGGGTGATAAATGACTTATAGCTTGTATACCTCTAGGTATGTACCC
TGCTATTTTTCGTAAGCTAGTAACTGATTTATGCCATTTATGTCACACCCGTTCAATAATT
TGCCTATTTGCAATTTGCTGTGATAGCGGCGGCGCAAGAAATTAGGAAGTATATAAAAAA
AATACAAAACCTTAATCTGAAATGGAATAGATAGCGTACCAACAGTATTTCTCGAGGACAGTTT
ACAGAAAGAAAAGCAACCGATGTTCAAGCATAGTACAGTATTTCTCGAGGACAGTTT
CTGCAAGATCGCTTACATTTGCTCTGAGAACATTTTACAAACGAGGCTCCCAAGATCTATA
TTTTTCCACAGGTGAGAACCTAGTTCGAACACCCCAATGATATAAATACTATTGTTAGATG
TTAAGGACCCCAAGGAAGTAAAGGATTAACAGTGCACCTCAATGATCAATAATTTCCGTTGA
ATAGTCCCTCTGGCGCTCTTGGATTGCCCGAAAAGAGTTTCAAGATTTTCCAAATTTG
CTAAACCACTCAGGATAAGAAATGATTTTCTTGTGCGAAAGGAGTAAAGAGCCAAA
TTGCCGAAGAGTTGGCTCGATCTTTATGGGTACGAAAACACTGGTATCTATCTCTGTTCTA
TTTACTGAGTGGTTAGCTTAAAGGTGGTGTGCTGAGCTTAAAGCCCAAAAAATAA

>YOR286W, 149 aa (SEQ ID NO 368)

MPFKSHSGILSRPSPTLVLRFTTTKAPKIYTFDQVRNLVEHPNDKLLVDVREPKEV
KDYKMPPTTINIPVNSARGALGLPEKHFHFQFAKPHDKELIFLCAKGVRAKTAELAR
SYGYENTGIYPGSITEMLAKGGADVKKPKX

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CTTCACTGTAAGTATCCGTCGATAGTAATCTTAACGAGATGATTTGATTAATCTCA
GGCGACAGCATGGAAATGGAATTTGACGCCCGACAGAGAGAAAGAGCGAAAGGAGG
AGGAAATATGAGAAACAACAGACTGGAAGATGTAAGTGAAGTGAAGGAGAGTAAAG
AGGAAATATGAGAGGAAAGAGGAGAGTAAATTAACAAGAGAGAGAGAGAGAGAAC
ATCAACAAAGAGGAGGAGAGTATGATGAGATGATGATTAAGAGAGAGAGAGAGAG
AAGAGATGATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
ATGATATATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
TTGATATATCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
TGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
ACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GCAACATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
GAAAGCTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
TTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
TAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

>YPL190C, 802 aa (SEQ ID NO 388)

MSDENHNSVVDIPSPELSDVSNSENELMNNSSADGIEFDAPEEREAREHEENEBOH
ELEEDVNDDEEEDKEKEBENGVEVINTEEBEEHQQKGDNDDEEDDEEDDEEDDDDD
DDDDDDDEEEDDEEEDGNDNSVGSDBAEDGEDBEKDKTKOXEELRRELTLEBOK
DVDEAIKKTIREENDNTHFPNMEVINYDLQKVYIMDSNMLNLPQFQHEPQEKMSA
ILAMLSNSTJALSVPFHDSTITTSASATSGASNDQRPPLSDAQRMRPRPLDLSK
PITBEEHDIRAAVYLHGENKITEMHNI PKRSRLFIGNLPKMN/SKEDLFRIFSYGHIIMQI
NTKNAFGFIOFDNFQSVDAIECESQEMFGKLLIEVSSSNARPFHDHDSNNSSTF
ISSAKRPFQESGDMDNDNGAYKRSRHTVSCNLFVRATDRYTAIEVFNPRFDSGTGL
ETDMIFLKPHEWELKLLINDAAVNGWGVVLNKTNRVNDVOTFYKGSQGEKFPFYSISIA
DDAVAFENNIKNNNNSRPTDYRAMSHQNPIMNYSYGRVQTSIPRPPPOOIPGYGRYO
PPQOQOQPYGNYGMPSPSHDQYGSQPIPMNYSYGRVQTSIPRPPPOOIPGYGRYO
AGPPEPQSPQIPMOQOQLSAILQNLPPNVVSNLMAQOQOQPHAQOQLVGLIQSMQOQ
APQOQOQLGYSNMSSSPPMSTMYNQNISAKPSAPMSHQPPPQOQOQOQOQOQOQOQ
QOQOQAGNNVQSLDLSLAKLOK

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>YPL201C, 1886 bp, CDS: 501-1886 (SEQ ID NO 389)
ATTTCATCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTATTTGTCGATATTTTCTTCCATTAACGATACGATGATGATGATGATGATGATGAT
ATTGGTGGCAACGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTTCTTTCGCAATTTGCCCTTTGATGATGATGATGATGATGATGATGATGATGAT
TTTTTACATATTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTGACGTCACCCCGCATTTCCGAGTTTCTTTTATTTATTTATTTATTTATTTATTTA
TCGCGGCTATTTGGTGGCCGGAATGATGATGATGATGATGATGATGATGATGATGAT
TACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGCAATTTTACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTTACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAAATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGATATTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGAAACGAAACGTAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GCCACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CCGTTTAAATTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AGATCTATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TAGACGAAAGCGTTCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT
TAGACGAAAGCGTTCAAAAGATGATGATGATGATGATGATGATGATGATGATGATGAT
CCAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATGCTTGAGAAACGAGACGTCATGATGATGATGATGATGATGATGATGATGATGATGAT
AACATCTCAACGAAACGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT
TGTTCTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACATTTCAACATTTCTTTAAATTA

>YPL201C, 461 aa (SEQ ID NO 390)

MGIRMOIYQDQKGVQFYHTRTYQWFDERSKYGNVYVNDYRPLPRTIKRHIDQ/FSNV
GEDGDVGNYSYEDDDGDEBEKLEDFVRSNRGLFVRINNYFTTHDQSPKSFENRSKY
WIFYSNOEDKRLLYDENQHLIFTKQFYQQLNLLSDAITCMQNPFGVNSVTIOILV
GFQNGKLLKNCNDANGVNNHLLKDPSTSSHSLILNVWAGLPHFVVSFLKDLGSD
ITSLDHQSNQSFQSFHNIDLPVLRITTTNVKSVLNFPOFTLYKQNDMLFHCRLGLSD
ASTLKEINFLKIDEDVQKIDYLLKTNHLLIETNNRYLSIPRDPLENSNSPVPVSDSE
VYPIFYKQELHVAHSGTGRIANNGKYIFITEQHLXGTLASVYKYSISFRKMLFGVSD
IRAKYGISVVDLPVGNCSVNSPVLITLDDNNIQTILK

>YPR028W, 1176 bp, exon1: 501-551, intron1: 552-684, exon2:

685-1176 (SEQ ID NO 393)

ACAACCCCTGTCATCTCCTGAACAAACAAATTAAGTCTTGAAGAACCTTGAGAA
GTTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGCTGAGAGGAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAACTTACTTCAAGTCAAAAGATTTTCAATCCTGTTGATGATGATGATGATGATGAT
CCTTATTTTATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTCTTCTTCTGTCACGTCACAAAGGATGATGATGATGATGATGATGATGATGATGAT
AAAAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAATAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

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TTACGGTATAGATTAAAGTAACTAATTTTATATGACCCCTCAAAGGCCATTTGATTT
ATCTTCTAAAGCTGCTTTAGAACGACAGATCCCTCCGATGTCACCTATACATGGTAC
CATCTCGGTAGAGTGCATATATGATTTAGAAACAGATTAATATATCTCCGCCATATGA
TGCTTTTCCAAACAAGCTGTTTATAGAGATTAACGAAGAACAACCTTATCTTTTGGT
GCTCAATCGGTGTTTATTTATTTACCAAAATTTCTTCAATATACAGAGACGCCCTTA
GACGGTTACACAAGAGCCATTAAGATTTAAATCTTATATTTAGTAGGAAGTTTG
GTACGATCTAGTACTCTTTTACGAAACTTTGTAAACAACCAATTAATTTCTGACG
CCCTTGATGGTTATTAAGACAAGCTTGCAAGCTGAGCGTAAATATATGTTTCAC
ATACGAGAAAGATTAAAGCTTTTAAACAAGCAAGCTTAGAGAAACCCAGGCA
TATAAACAATTCGAAGGGTGGCCACGAATTCCTCTCTCTGCCCCCACTTC
CTGTGATTTTACAACCTTACTTACCAACTATATGATATCAAGGAATATCTTTTG
AACCTAGATTTCTAGCCCAAAATCTGCCAAATGGTACTTCTTGCACAAATGT
ACAATAGTGGAGCTTCCCTCTAAATTACAAGCTCAAGCTCAAGCTCAAGCT
CAAGCACAAGCTCAAGCACAAGCACAAGCCCTATTAACCTTCTTGCACAAATGT
AGCGCAGGCACAAGCACAAGCAGCGCGAAGCACAGGCCACAGGCACAAG
CACAGGCACATGCAAGCGCAAGCACAAGCACAAGCACAAGCACAAGCACA
CAAGCAGCGCGCGGCACACACAACACAACAACAACAAGCAACAACAACA
ACAACAACAACAACAACAACAACAACAACAACAACAACAACAACAACA
AGCGCAGGCATTTACAGGCCCTTACCAAGCACAAGCTGCAGCAAAAAGGA
GTTTCTGCTCAATATGTTTAAATCTTCAACAAGGCCATATATATACACACA
GCCAACAGTCAATACAGCTACCACTTCAAGCCAGCCTCAAGCCTCAAGCTCA
TGGAACATCCGCAAGCTCTCAACTCGCCACCTCAACAGCAACAACATACAA
TCTGTTTCAACATCTCAACACACTCAAGGCCAGCCTCAAGCCTCAAGCTCA
CCAACTTTTATCCAGCATTAAGCTGGAAGCAGAACGTTTCTCTCAAGA
GATACATGAAGGTGCATCTCACACTTTATGATAGATGTCGCCGTTATCCAGT
AGCACCCACACAGAGATTAACAACAAGTCTCTCTGCTCAACCAACCCATGCG
CATTTCAAGCAAGCTCCGCAACAGAAATACAGAACCTCGAACCCACAGG
TAATGAGCAACAAGTTGAACTCTCCAAATTTCAAACATCAACAATATGTA
AATACTGCTACTTTCTCANTGAAGAAATGCAAACTGAGGTGAGCGACCA
ATCGCCGACGATGTTGGAGTCTAATACCATTAATTACTTCAACAAGAAAGA
AACCTGTAAAGCAAACTCAATTAACCTTCAAGTAAATTTGGCGCAACAGGACCT
CCAACAGGAAGTGTCTCTGAGAGAGCTCAAAAGCAGCTTCTGTTTTC
CTCTTCTACAAACAACCGTTTATACGGAACCAAGACTCATCTAGTGTCCAAAG
CAACTGTATCATCAGAAAGTTTCAACAACAAGCAAAATGACCAAAAGCACT
GCTGAGACCAATAGAACTTTTACTGCTACTGTTCTCTGAGAGAAAGCAAGGCC
TCAGTAAGACAGAAAGTACAGCATTTCTTTAAAGAGAAACAAGCCCAACATG
AAGACTTCTGCACCTTACTAGAGAGGCGGAGCCACAGCTTCCACAGAT
GCTGAAAAACAACAAGATGAACCCGCTGCTACACGATTAATGTTAATCA
ACCTACTTTTGGAAACAATGGAACAAGTGAAGAGGAGGCCAAATATCGCTG
AGGAAGCAACCAACTCTCTCAAGAAATAATCCCAAGGAGAAACACATCTCA
ACGAAGAATCAAGCTAAGSCAATGTTGAAGAGAGATGAACATACAGCAGCACTCA

YBR112C. 966 aa (SEO ID NO 52)

[illegible]

A

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[illegible]

YMR043W, 1361 bp, CDS: 501-1361 (Seq ID NO 305)

AAGCTGTGCCAAACAAGGTCATCTCTCAATACTTACCAAAAAGCTGAGGCG
GTACTGTACTGGAACTCTGCTCTTTCTTACCTTACTCTCAATTTGGCTT
TGTCTGCTTTTACGATCTGTTTCTGGCGGTCTGCTGTTTCTTTTATTA
CTCTGCTTGTGAATATTTCTTCTAAGTATATATACATATCTATCATCGCA
TACCCAATCGGTTTCCCTATCTCTCACCACTTTTTCCTGGAATAACATATAG
CTTAACAAGCAATTTTATTTTACGTTTGTGTAAATTCATTAATCTGATTAATG
TTTTTGAATTTTCTTTTGTGATCATATTTTATTAATCGCTGTTTATGTA
CTGTTTCTTCGATTTACGTTATAGGGAATAAAGCGGAAAGGAAAGAGAA
AAAAAAATTAGTCGAGCAATAAGAAGCGGAAAAACAATAAAAGTTTGTG
GATCTCAAGACTTCTGTCTACGCAACAATATATATAGCCACCCAGCAAGA
ATGTCAGACATCGAAGAGTAGGCTACTAATATATGGCAACGAAAGAA
GAGAAAGAATATAGAAATTTAAGTCTCATCGAATAAAACATAGGCGCCATG
TGACATTTTCCAAAAGGAAGCAGGTTATCATGAAAAGGCGTTTTCAGCTTT
TCTGTCTTAAACGGGACCCAGCTGTTGTAGTCTTTTTCAGAAACAGGGG
TTTGGTATATACTTTTCCACGCCGAGTTTGAACCTATAGTTCACGCAAC
AGGAAGTATAGAAACCTGATCTCAGGCTGTCTTAAACGCCCTCATGATGAG
GAAGAAGCAGGAGGAGAGACGGTATGATGATGATGATGATGATGATGATG
TGTTAATGATATCAACGCCACCAACAACAGCAACAGCAACCAACAACA
AGCAACAAGATTGGAATGCGCACAGGCAATAGCTTTAGGCGCATCTTAATCAA
GATCAAGTACCGGCACGGCGCTGAAACAAGAGGTGTAAGTCTCAATATGCT
AGCGGTTGCCAATCTCTATATCAAAACTAATGATTTCAACAGCAGCAACATC
ACACGCAAGATTCAACAACAACAGCAACAGCAACAGCAACACCAACAGGAG
CAATATGTCACAGCAACAATGTCTACAGCATCTCCGACCAACAGCAAGGAAT
ACCCATCTCGCAACAATTCGACGCCACAGCAACAGCAACAGCAACAACA
AACTGCAACAGCAGCAACAGCAGCAACACACACACCCCTTCACCGGCAATT
CATCAGCTCTCAACAGGCTTTTGCCAAAGCTGCTCCCTCATCTGAA
TGCTGAACATGAATGCTGCTCTACCAATATCTTTCAAGAACCGCAACAG
GCCAATCTAA

YMR043W. 286 aa (SEO ID NO 306)

[illegible]

VPI.089C. 2531 bp. CDS: 501-2531 (SEO ID NO 385)

TTTCCAGGCT, 2331 bp, GDS: 301-2222 (GDB: 389696).
 TTTCCAGGCTGCGAAAATAACTTCTTCCAGGTACGAAAGTGTGTCTCAGTCTG
 TATATTAAATGCGAATAATCGTCTTATATTATGGCTCTCTTAAACGGCG
 CAGCATCACCGGGTGTGAATGCCAATCCGCGAAGAAGAAAAAATT
 TACCTTCAGATTCTGATTAATAAATCCGAAAGATGAAGTAAATTAAT
 AGAAACAGCTCGATTCTTCTCTGACACATAATTAATTAAGGACACAGAAA
 AAGAAAGCTGTAAGAAAGACGAGCGCTGTCTTAAAGTGTTCACGACTGAT
 TCTAATTAGAAAGTCCCTACTCTGCTGAGGCAACTCAACTCTCTGCTGTTA

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NPQQQNVFNVNLDNNLLKSNKGTTPSSCTGAFSRTPLSKIDNMLMFNQP
LPTSPSRFSSLSLTPPYGRKILNDVGPVAKALISNSALVDFQKARKOI
TTWATSTGLENNILQRTPLRSNNKKLFIKTPQDFTINSTLTOKENK
QDIYGSPTTTLQNLSSISIKSLDMSRIPLASRSNLDLSNVDDQLFD
LGLTRLPLSPNPNCSLHSTTGTSLAQIPELPMGSRFSDTGINPISSS
NTVSFKSGNNNSKGRITKQNGKPKSPFOIIVANIQFNQDTSSSLSS
LNASSSAGNSNVTKKRAKSLKRSQSLSDSGSKSQARKSCNSKNGNL
FNSQ

YDR224C, 896 bp, CDS: 501-896 (SEQ ID NO 111)
TTTCTTCAACACGACGAGTAACTATGTGTCTCTTTTGTGACCCACCA
AATPACACTCCATCCAAATGCTCCGACAGTGGCGGAAATTTTGAAC
AGCGCTAATGAATTTGTGTAGCTCGGCGAGTCAATTTGAAGAAAC
CGGTTGGGTCTTAACTCTGGTGTAGACCTCAATGTCCGCCAAAGGA
AGCTGTCTCACTTTTTCGGCGTGTGACCCCTTTCTCCGGGAAAATAT
GAGAAGCATGGATTTAAATCAAGAGATTTGGCTTAGTAGTGCAATTA
CTACCTTGGTGTGTTACTTGTAAACATGATTTGATCATCTCAGATGCTCAG
TTTCTTGTGTATATAAACAACATGATTTGATCATCTCAGATGCTCAG
TTTATAAGACGTTTCTCTTTCGGCATTTTCGATTTATTTATATAA
TTTATCTCTATACAGCAAGTCAAAACCAACAATAAACCATACACATACA
ATGTCGTGCTAAAGCCGAAAGAACCTCCCAAGCCCGACGTGAATA
GAAACGCGCTAAAAGACTTCCACTTCCACTGATGTGTAAGAGAA
GCAAGCTAGAAGGAACATACCTCTCTTACATTTTACAAGTTTGAAG
CAAACTCACTGACACTGTTTTCGAAAGTTCGCTACTGAACTCTCTTGA
CTCTTCTGTTAAGATATCTTGAAGTTCGCTACTGAACTCTCTTGA
TGGCTGCTGATATCAAGAGTATCTCTGCTAGAGAAATTCAAACC
GCTGTAGATGATCTTACAGAGTGAATGGCTAAGCATGCTGCTCTGA
AGGTACTAGAGCTTTTACCAAGTACTCTCTCTCTACTCAAGCATAA

YDR224C, 131 aa (SEQ ID NO 112)
MSAKAEKPKAPAEKPKPAKKTSTSDGKKRSKARKETVSSYTKVLK
QTHPTDGIQSKNSILNSFVNDIFERIANTEASKLAAYNKKSTISAREIQT
AVRLTLPGELAHVSEGTAVTKYSSTQA

YLR294C, 830 bp, CDS: 501-830 (SEQ ID NO 281)
ACCAACCACTTCTCTTGTCTCTCAATATCAAGAAATCAAGAAATCAAG
CCACTGCTCAGATGTTATAGGAAGGGGTGTAATTTATATACAGGTTCA
TCTACCACTGACCAAGTCCATACAACTTGAACCTCTCGGTACCACTCT
AATCAAAATGTTCCCTATGCTTCCAGAGATATCTGCTCAATGCTTCAG
TTCCTCCATTTGAGACTGTGCAATAGAAATTTCACTACCACAGATATCC
TACAACGTCATCAAGATTTGTATTTTGGGGAATCAAGAGACACCAAACT
GGCTCCAAAGTCTTCAAGATGCTGAAGTAAATGTTTGAAGCTTGAAC
CACCACAAAACCAAACTTACCAAGAAATTTGAACCTCAAGGCCCTGGAAC
TTAAAGGCTTACCCGAGCAAAATAGAACTGCTCATGTTGCTTAAAGA
GTCTGAAGAGGTGAGTACAGCAATTTGAAGAGATTTGGCTAGTTTGG
ATGATAGGAGGAAACCAAGAAAGTCAATTTGAATTTTCAATAGATCTCT
CTTGTCAAGAAAAAACAACAGAACCAAGCTGAAACAGATCATATTAT
TTTGGCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
AAAAGGCAAAATACATACGCACTCTTTTGAATTCGAATCCAGTACAAAG
GAATTTAAATTTAAACAAATAACAATTTGATACATAGACAGCTCTTAT
CTTCTCTATTACTACTATCTTTTATTTTCAATTAATTAATTAATTAAT
ATGACCTACGCTCTCTTGTGTAATAATAA

YLR294C, 109aa (SEQ ID NO 282)
MLMKPKVIELFIASSLSKKKQEPQAEQDHYFWLSSHLFIPESSTIK
KKQNTLRLCNPQHPKMQNLFFKQIKIQLYIDTSLSLFLLLLFFFYNNYFLS

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MTVASLVNK

YMR256C, 683 bp, CDS: 501-683 (SEQ ID NO 319)
CTTTTCACTATTTTACCTTCTCTCTCTCACCTGTAAATATTTGTGTCT
ATACACACCGCTAAAAACCTTTTGCATCACTTATACCTTACATTTCTATA
GACGCTATTTTGAACAGATGTAACCTCTTTTCTTTTCTTTTGTAGTTTGA
TTGTACTCTGTAAGAGTACGCTTTTATTTTATTTTCAATTTTATTTCTTC
ATACCATGTAAATATAAAGCGCATATAATCACTACCTACCTTGTACAGCTA
GAATTGCTGAGCTTACAAATTTGCTTTTATTTTGTATATATATGACGATATA
CATATAGTGTACGAAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
GCGCATCTCGGAGAAATTCGGCTGTGGGAGGAGGTTTGAAGAGCGG
ATAGAAATATAAGATGATATTTATTTATTTATTTATTTATTTATTTATTT
GATATAAGATTCTTAAACCAAGATACAGAAAGCAAAACAAATAATAATA
ATGGCTTAATAAGTTTCAACTACAGAAATTTTCCAACTTCCACTAA
ACTCTATGTTGGAGACATCCAAAGGTGAGCTTTATPACCTGTATCCATTTT
ATGCTATTTTGTGGTAGCGCTGCTTACACCACTTCTATATACATTTCCAAAT
GCTATTAGAGGTATCAAGCCCAAGAGGCATAG

YMR256C, 60 aa (SEQ ID NO 320)
MANKVIQLQKIFQSTKPLMWRHPRSRALYFFVAIFAFAVVVTPLLYIPN
AIRGIKAKKA

YLR327C, 761 bp, CDS: 501-761 (SEQ ID NO 287)
TTCTCATAGCTATGTTTTTTGTAGTATGACCTTCTTGTCCACAGTAA
TGTGGCGGGAAGATGTTGAGCTAGCCCGTGCACAGTGAAGAGAGACGGA
GGCATTTGTGGGTTTATCTCGGATTTGCGGGAAGAGGCCCTTACACCTG
TTGACCAACCCCTCTCAGAGTAAATTTACACAAACAGTGGTGGTGCCT
TATGCTGTATACGAGATGATGATAGAGCTGCTGATTTGGGTGAGAAAT
TTTGTAGGCTTTATGGATATGGTATGGTATGGTATGGCTTGGGTGAGT
TAATCAGACACCACTGGAATATATATAAGAGAGAGTCTTGGCAGGTA
GATTTGACTCTCTCTACACTTCTTCTCTCTTTTATTTATTTATTTATTT
TTTATTAAGCACAGCAAAACGTTAAATAAATCTAATAAGATTTCATT
ATAACATTAACATTAAGCACAAATTTTAAACAAACAAACAAATTTCAAAAC
ATGACCAAGACTAGCAAAATGGACAGTCCAGAAAGCAAGTCTTAACCCAA
GTATTTACCCATAAGGCACTTTTGGGAGTCTCCCAACCAACAGCTCAAGA
GAGAGCTATGGGAAAGCAATTTGGGCAAGCTTCCGAGTGAATTAAT
GACTTAATGATTTCTGGGCAATTAAGACAGTCTTCAACAAAGACCAAGAG
GGCTCTAACTCCCAAAACAATCAAGAAAGGCTTTCTGATTTGCAACAAAT
ACCAATCTAA

YLR327C, 86 aa (SEQ ID NO 288)
MTRTSKMTVHEAKSNPKYFTHNGFGEPSNHVKRGYKGNWKGKPGDEIN
DLIDSGLKTVFNTRGRSNNQNNRRLSDLQYHI

YHR161C, 2414 bp, CDS: 501-2414 (SEQ ID NO 211)
GTCAATGCGCAATAGGAAAGCGCAAGCAAAATGATGATTAATTCGTAGGA
AACATGCGCCCTCAGGCTGAGCACTGACGTACTGACCTGGCTTTT
GTAGAAAAGATGACCCCTGCGAGAGAGTGGGGAATTTGAGGGGTCTT
CGCTACCCCTTAAATGTAAGAAATATGATGAAGAATATGATGATTAAC
TCTTGAAGCGCGGGGTTCATCACTTTTACGGATTTGGTGAACACA
GGGGCTCAGTTCGATATGATGATTTAGGCTTCCAGCGTGGTGGTATTC
AGTTAGCGGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GTTAGGTGAATGAGTAGGATGATGATGATGATGATGATGATGATGATGATGAT
CGTCTTTTGTGGGAGGAGGAGCAAAACCTCTCTCTCTCTCTCTCTCTCTCT
GACTGTTGATATCGGAGATCTAGAGTATAAATTTGATTTGAGGCGAG
ATGACAAACATATTTCAAGTTGGTAAAGGCTGCTACCAAGATCAAGTCAGC

CCGCCCAACAGAGATCTGATCCGATCTCTTGGGGACCGAGATG
AAGAAGATTTCTATGATATCGAAGGGTTGGATTCCGAATTAATGAC
ACGGCGTGGACTATATGATTAATCGCTTTGGTGCTTCAATTTGATGAT
AAGGAGGGTCCAAAGATGTGATTCATTCGGTATCACTTAGAACCTGG
AGTTTGTGACATTTGAAACATACGTGGCTCCAAATGGAGTGGCTGAG
GACATGAGGGCACTTGATAGATACGATTAATTTGAGGTGATGACAC
GGAGTTTGGTAAATCAAAAAGGACTATGAGAGCGGCTATCCGACACT
TGAAGCTGACAGTGCATTAACGAGTCCGAAACAAAGCAAGCACTCT
ATCATATATGACATGATATGATGGAGTCCCTAGAGGTATCAATGATCA
CCGATTTAAACAGTATACACATATGATTTGATGATACGATGATGATCA
TATTTGGTTTCAAGTCTTATTCAGACCTGAGGCTATTTTTCGACATCTCA
CTCAACGAGGATCATACTCTGCTGAGATCTTTTTCGACATATTAATGCT
TCATATATGACAGATCTGATACCTGATACAGATCTTGTGATTTGATGA
CCGAGCAGTGTGAGTACTTGAAGCGGGAAGACTGCGGGCTTGAAA
ATACCCTGATCAAGATATCACTACCAATGGTCAATCGCTAGAGAGA
ACATCTGATAGAGATGATTAAGACGCAAACTTTTGTGCGCTTGACA
GTTCTCAAGGAAGTGTGGGGCGCTAGTACGCAATTAAGGCAATTTGAA
AATCTGAGCAATTCGGGAAACAAAAGGATCTAGAGGCAATTTGAA
AATCTTACCAACCGTTTGGAAACAGACTCTTATGATATCTAATTTGATC
ATGGCTGTGGCTTATCAACAGCAAGATGCAATTAACCATTTGATATC
TCAAACTCAGCCACAGGTGATTAATACCAACCGCTCAATACAGTGAATTC
CAAAATTTAAACGTTCCGATATGATGATGATGATGATGATGATGATGAT
AACCTGTATCAAGATGATGATGATGATGATGATGATGATGATGATGAT
GATTTAAACCATTTTACAGATCACTGCTGCTGATTAATCAACATGCTCAT
ACTGCTTCTACAGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
TGCACAACCTGCTTCTAACAACCGCTGCTGCTGCTGCTGCTGCTGCTGCT
TCGACAACCTGCTTCTAACAACCGCTGCTGCTGCTGCTGCTGCTGCTGCT
CGCAACAGGATCTTGCACACGAAATATGCTTAAATTAACCATTTTAC
GACCAACTTTTGAACAAATTAACCAATATGCTGCTGCTGCTGCTGCTGCT
ATCAAAATGCTTCTTGAACCAATTAACCAATTAACCAATTAACCAATTA
ACAAATATGCTTCTTGAACCAATTAACCAATTAACCAATTAACCAATTA
GATGCAAGGATGATGATTAATTTCTGAGCTTGAATTAATTAATTAATTA
CAGGCTCACTACCTGATCAATCTTCCAAACAGCAATTAATTAATTAATTA
GCAACAAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCA
CTGCAACTGCAAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAG
CTCTCAAAATTTTCCCTTCTATCAACAGCAACAGCAACAGCAACAGCA
TCAACACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAT
TAATGATATGATA

YHR161C, 637 aa (SEQ ID NO 212)

MTTYFKLVKATKIKSAPKQKIDLPILDTLSNEEDFYEIVKGLDSRIND
TAMTIVKSLVHLMIRGSKDVALRYSRNLEFDIENIRGNSGASG
DMRLADRYDNYLKVRCREFGKIKKDVRODVRTLKLSNYSRNKXHS
INILADHVESLEVOIALIKNKTYOJLSNELIIFPKLLIQDLIALYNA
LNEGIIITLESFELSHNAERFLDYKTFVDLFEHVRYLKSGETAELK
IPIKIHITTKLVRSLEHLEIDDKTNHTVYVDSQSGAGAVAVAKSTNOE
RLEQIREQRILEAOLKNEQVAVSALPTVTAQSYNPFETDSNHTNP
MAVANQTOQIANNPVSOTQPVQWNTPTAHTERANLPEVAAVQHTNPF
NPVQAGVSAQOTGVYSINNHLPPTFGAGFGGVSQDTTAAASQOVSH
SOTGSNNPFLAHNAATLATNPFAHENVLANPFSRPNPDEQNTMMPLQOI
ISNPNQNTYNOQPFQOQKMLPSSINSVTPTSNQSGSNITPQRDKIEF
QAHYQNHLDQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ
PONFPFYPOQOPQPEQSQTOQPVLGNOYANNLNLIDM

YLR206W, 2342 bp, CDS: 501-2342 (SEQ ID NO 277)
TACACCTGACTTCCCATCATACAGACGATGCTGATGAACCTTGACAC

CGCAGCTGTTAGTAAACAGTGCAGCCCAAGATCACATACCGAAGGGC
GATATCACACTCAGTATTTCTACATCGACATAGGGTATGCTGGCAGTA
TCCCGACAGATCCCATTTGATTTGTTTCTCCAAACCGCATTTTATSTGATAC
GATTTATCTGATATACATGGCTTACAAAGAAATTAACCTGGGGCGAAGGT
GAAAAAATAGTACAGTAACTAAGAAAGAAAGATTTAGTTACGAGACC
TTTCAAGATTCACACATCCCAATATTTTGTCTATCATTAATGACCTTGT
TGAAGAGGGGCTGCTTTATTTATTAATTTTCTGTTTCTGTTTCTTCAAC
TGCATATGACATTTAAGTATGACCTTCAACAAATTCATATCATCTT
CTTTTCTTTATTTTGAACACCTTCTGCAAGAAAGATGAAAGGCTACTC
ATGCTCTAGCAGTTTGTGCTGCTGCAAGAAAGATGAAAGGCTACTC
ATCCACAAAGTCTTGTGAGATATCCACGGCGAAGCATCTGAGAGACTC
CATCTATGACACTCTGACAGATTTGGCAAGAGCTGAAACGATTAAGGG
GACTTCTGAGATTAATGATATGTTAGCAAGAGCTGAAACGATTAAGGG
CAATATCTGAGACAGCTTGCATATGCTGACAGTGTGAGACTTCTG
TTGCTTGGGAGTGAAGACTGTGCTATATGCTGAGAGAAATTTTTC
GTAATTTAGACATTTAAGGAATTCAGACAGAAATGAGTCCGATTTGA
CGAGGACAAATTTATCAGATTAAGGCTAAAGACTCGTCTCTTGTGTA
ATGATGAAGAAAGGCTACCGAAGAGGCTATGATTAACAGAAACAGAG
AGGGCAACAGAGCTGTAGGCAAGGCAAGCAAGAAAGAAAGGAGAG
CAACCCACAGATTTCTTCTTCTTACAGAGCATTTGAAAGGAGGAG
TAGAGAGAGCAGATTAATCTGCTCAAGAAATGAACAAGCTGCTTGAAGAA
CTGGCCCAATGACAGATGAGATGCTGATCTTCAAGCTGCTTGAACAT
AAGTAAAGAAAGAGAGGTTGAAGCAATTCGAGGAATCTAGAGATTAAC
AGTAAAGCAACAGCTCTGCTCAATTTCAATTTGATATCTTCAACAGAA
CAACCAACAGCAACAGCTGATACGATTAACAGAGCAAGAGCAAGAGCA
CCAGATATATCTTACAGTATACGATTAACAGAGCAAGAGCAAGAGCA
TGCGTACAGAAAGATGCTGAGCAAGCAAGAGCAAGAGCAAGAGCAAG
GAACAAATATTTTACAGAGCAACAGAGCTGCGGGCGCTTCTGCTG
CTTGCACAGCAACAGAGCGCTTATATGCAACAAACAGCAACAGAGC
CCGGTATTTTCAACACCTTGTCTGACAGGTTCTAATATTCGGTTTCC
ATGATTAATTTTGAAGAAAGCAAGAGCAAGAGCAAGAGCAAGAGCAAC
AAGCAACAGAAAGAGGATGACACACAGAAATTAACAGAGAGGCAAC
AATTCGAAAGCAATTAACAGAGCAAGAGCAAGAGCAAGAGCAAGAGC
GAAAGAGCCCAATTAACAGAGCAAGAGCAAGAGCAAGAGCAAGAGC
CCAATTCGCAAGCAACAGAGCAAGAGCAAGAGCAAGAGCAAGAGC
CTATATTCGATTAATACAGGATTTGAATACCTTGTAGCAACTGTGCA
GGGATTAATTAATTAATTTCTGAGGATACAGGCTTCTGCAACAGCA
TACAAAGACAGGACATTTTAATTTCTGAGGATACAGGCTTCTGCAACAG
TTACTTAATGAAACCAAGAACAGCTTCTTCTTGAACCAATTAACAGCT
TACCAAGCAACAAATATGCTGCGCAGCAACAGGATACGGGTTACGGT
CCAACCTCAAGCTCTCTCTACTATTTCTCTCAGCAAAATCTTACTGTGA
TAAAGTACTCTGAGCCCAACAGCAACAGCAACAGCAACAGCAACAGCA
TACATGCAAAATTTTCAACAGCAACAGCAACAGCAACAGCAACAGCA
ACACACACCAATTAACAGCAACAGCAACAGCAACAGCAACAGCAACAG
AACCTATCAACACCAACAGCAACAGCAACAGCAACAGCAACAGCAACAG
GGATTAATCTCTGACCAAGGCTTAAATTTGATCTTTTGA

YLR206W, 613 aa (SEQ ID NO 278)

MSKQFVMSAKRMKGYSTQVLVNDATANDSTRPSTIDLDLAQRSDYS
DFEIMVMDLRKLDKGVKRWVAKSLTVLDLVRFSGSENCVIMGCFNY
VITLITREFRHENESFDEGOILIRVAKELVSLINDEERLEESNMTNR
RANRAARPRRQRQSNPHDSPSYODLEKALEBSRTTAAQEDQRRRE
LAQYDDEDPDFQALQLSKEEELKQDELQNLQKQOQSLSPQAPLPQOQ
QPOQOQPAYVDIFGNPISODEYLQYQYQDOEQMAQQRWLDQOQEQOQLA
EQQYFQOQOQAAAAAASALDQOQTAANMQOQOQOQPADFOQLPTGSNNPFS
MDNLERQKQEQHQLQRQEBARQOQEQDLKQLQDLQRQOQEBQJLHQRQ

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EEALQ00QAQLLQ0QAQFQ00QPLQKQRTGNGQSDKSYSDLNTLLATGT
GIDFGNTEGARIQAHTKTGTFINSGCTGYQKVWNEKNNPFLSNQVYG
LPSTNIVPTQSGRGNOFQSPSTNSPQNPTGTSYSGFQ000QFQ00QFQ
WQNFQ00Q0QYAQNFQ00QPYQTYNQ00QPYIQHQQ000000000000
GYTPDQGSGLDL

YDR342C, 2213 bp, CDS: 501-2213 (SEQ ID NO 119)

CAC TTC TCAGAAATGAGTCCAGTGGCAGCAGCTAAATTCGAAAAAATTCCT
CCAGAAAGGCAAGCCAAATTTTTTTTCAGGGAATAAATCTTTTCTTAGAC
CCACTACTTTCGTAGGAACAATTTTCGGGCCCTCGCTGTCTTCGTAGG
TTCATCTTTACATTTGCTTCTGCTGGATAATTTTCAGAGGCAACAAGGA
AAAATAGATGGCAAAAGCTGCTTTCTCAGGAAAAATCCCCACATCTT
TCGAGATCCCTGTACTTATTTGGCAACTCAAGAGATGAAGAGGAGAA
ATCAAAATCTTAGACTAGAACTGAAAAAGAAATATAAATAGAGACGATA
TATGCCAATACTTCACAATGTTTCGAATCTATCTTCTCATTTTCGACGTATTG
TAAATAATAAACAATCAGAGAACAAACAAGCTCAACTGTCTTTCTTCAAG
AACAGAATAACACAAAAACAAAAGTTTTTTTAAATTAATCAAAAA
ATGTCACAAAGAGTCTGCTATTCGACAGAAACCTCTCTGAGCATCTC
TGCCTTGACTACGCTCCCACTCGGTTTTTATCTACACATCAACAAGG
CTGAAGAAGATTGAATAAAGCTATGCTGAAGGTGAAGACACGAACCT
GTCTGTGAATTTCCAAAGAGACCGAGTCTTCGCTTGTCTACTGCTCAT
TATGTGTATCATGATCGCCTTTGGTGGTTTCGTTTTCGTTGGGACTATG
GTACCAATTCCTGGTTTCATCAATCAACACCGATTTTCATCAGAAATTTGGT
ATGAAGCATAAAGATGGTACTAATTAATTTGTCACAGGTAGAACTGGTTT
GATTTCTCACTATTTTCAACTGGTTCGCCATTTGGTGGTATGATCTTTT
CCAAATTTGGGTGATATGATACGGCTGCTAAGTGGGTGATATGATCTTT
GTCACTACATCATACGGTATTAATTAATTCATAATGTCATCTATCAACAATG
GTACCAATTTCTACGGTAGAATTAATTTTCGGGTTCGGCTGGTGGTGA
TTCCGCTTTATCTCTATGTTGATTTCTGAAAGTATCCCAAGCATTTA
AGGGGTACTTTAGTCTCTGCTACCAATGATGATTACTTGCCTGTCTT
CTTGGGTTCTGTACCAACTTCGGTACTAAGAATCTTCCAACTGTCTGTC
AATGGAGAGTCCATAGGTTTGTGTTTGGCTTCGGGCTTTGTTTATGAT
GGTGGTATGACATTTGTTCCAGAGTCTCCACATTAATTTGGCTCAAGTCGG
TAAGATCGAAGAGCCAAACGTTCTTATTCGCCGTTCTAACAAAGTTGCTG
TTGATGATCCATCTTTTGGCTGAAGTCTGAAGCTGCTTTGGCTGGTGA
GAGGCAGAGAAATAGTGGTAAATGCATCTCGGGGTGAATGTTTATGATG
CAAGCAAGAGTCTCTACGCTGTGATCATGGGTGCTATGATTAACAATCT
TACAACAATTTACAGAGTGATAACTATTTCTCTACTATGCGTACTACTATT
TTAAGGCTCTGGTTTGGTGGTACTTTTCGAAAGCTCAATTGTTCTGTGGG
TTATGCTTTAGCTTTCTCCCACTTTGTTGGTATTTACGTTTGTGACAGAT
ATGGTCTGTACTTTGCTATTCGTTGGGTGCTCACAGATTAATGCCAATGGTCA
ATGTTGTGCTATGCTCTCGTGGGTGCTCACAGATTAATGCCAATGGTCA
AGACCAACCATCTTCCAAAGGTGCTGGTAACTGATGATGTTCTTTGCGCT
GTTCTCTATATTTCTTGGTCTACTACATGGGCTCCAATTCCTTATGTC
GTTGTTTCGAAACTTTTCCCATGAGAGTCAAGTCTTAAGGGCTATGTCAT
TGCTACAGCTGCTAATTTGTTGGGTTTCTTGATTTGGTTTCTTCACTC
CATTTATCTGGTGTATTAACTTCTACTTACGTTTACGTTTCTCAATGGC
TGTTTGGTCTACATGTTCTATGTTTGTAGTTTGTCTTCCAGAACTAA
GGGTTTGACTTTGGAAGAGTCAACACATGTTGGGAAGAGGTGTTCTAC
CATGGAAGTCTGCTCATGGTCTCCACCATCCAGAAGAGGTGCCAATCTAC
GAGCTCAAGAAATGACTACGATGACAAGCCATTTGTACAGAGAAATGTT
CAGCCACCAATAA

YDR342C, 570 aa (SEQ ID NO 120)
MSQDAIAIEQTPVEHLASVDSSASHSVLSTPSNKAERDEIKAYGCECEHEP
VVEIPKRPASAVTVTSIMCIMIAPFGGEVFGWDTGTISGINQTDFTIRRFG

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MKKHDDNNYL SKVTRGLIVSIFNIGCAIGGIIISKLGDWGRKUGLIVV
 VYIIGIIQIQTASINKWQYPIGRISLGVGGTIAVLSPMLISEVSPKHL
 RGTLVSCYQLMATTAGIFPGYCTNFCNTKNSYNSQWRVPLGLICPAWALFMI
 GCMTFVPSRPLYLAEKKEIKERAKISVKNVAVDDPSYLAEEVAVLAGV
 EAEKLAGNASNGELFSSKTKVLQRLIMGAMQTSQLGDIWVFFYCYGTTI
 FKAVALSDSFETSIVLGTINFASTFTVGVTVYVERGRRCTKLWGAASMTAC
 MVVYASGVTRLWPNQDQPSKGAGNCNIVPACFYIFCPATTHAPIPVV
 VVSEFTPLRVKSKAMSTATATIANMLWGFLIGFTFPTITCAINFYCYGVFMG
 CLWPMFFPVTSTKGLTTLBEVNTWMBEGLVPKWSASWVPPSSRGANY
 DAEENTHDDKPLXYRMPSTK

YDR343C, 2213 bp, CDS: 501-2213 (SEQ ID NO 121)

AAAAAAAAATGTTTATTTAGGCAACGGAGATTGCTTTTATCCACGTTTACCCCC
ACAAAATGTCAGGTACATATTTGGGCGCGGCACTGCAAAACCAAGTTTATT
TTCTTTTAAACCGCTGGAAAAAAGAGAAATATTTTGAATTTGTCGAGAGA
ATATGTCGTAGGCAAAATTTGAATTTGTTCTTAAAAAATTTCTTTGTATAC
TCAATTGAGATTATTTACAGATGCCCTCCGTGCGCTTCATTGAAAAAATCCAA
GAGATGTCCTGGATCTGTATAGCAGATTTTGGCTTCGACACAATAGGAGANG
AAATGGCTATACATATATAGAAGACACATATATATAAAGAGATCTGAT
AAAAGACATATGGTTTGTATCATCTCTCTTCTTTTCCAAATTTTCTGT
TTTAAATAATAAAAAACAAGAACAAACAGCTCAACTGTCTTTTCTTAAG
ACAAAGAAATGACCAAAAAACAAAAGTTTATTTAAATTTAAATCAAAAA
ATGTCACAAGACGCTGCTATTTGCAGACAAATCTCTGTGGAGCAATCAAGG
TGTGTTGTACTACGCTCCCACTCGGTTTATCTACCAATCAAAACAAGCT
CTGAAGAGATGAATAAAAGCTTATGTGAAGGTGAAGACGACGAACCT
GTCTGTTGAAATTCAAAGAGACAGCTTCTGCTATGTCACTGCTCTCTAT
TATGTGTAATCATGATCGCTTTGGTGGTTTCTGTTCCGGTGGGATACTGT
GTACCAATTTCTGGTTTCAATCAACAAACGCAATTTTCCGGTGGGATTTGCT
GATACGCAATAAGATGTTACTAATATTTTGTCTAAGGTTTGAACCTGGTTT
GTATGTTCTCAATTTCAACATTTGGTTTGGTCTGCCATTTGTGTTATTTCTT
CCAAATTTGGGTGATATGTAATCGTTCGTAAAGTGGTGTGATTTGCTGTT
GTCACTACATCACTCGGTATATTTATTTACAAATTCGACTATCAACAATAAT
GTACCAATATTTCAATCGGTAGAAATATTTTCCGGTTTGGGTGTTGGTGTA
TTGCCCTTTATCTCTATGTTGATTTCTGAATTTCCCAAGCAATTTA
AGSGGTACTTTAGTCTTCTGCTACCAATGTGATATCTCCCGGATATTT
CTTGGGTTACTGTACCAACTTTCCGTACTAAGAACTACTCTCAACTCTGTGC
AATGGAGAGTTTCAATATAGTTTGTGTTTGGTTCCTGGGCTTTGTTATGATT
GGTGATGACATATTTGTCAGAGTCTCCAGCTTATTTTGGCTTGGCTTATGATT
TAAAGATCGAAGAACCAACAGCTCTATTCGCGTTCCTAACAGGTTGCTG
TTGATGATCCATCTGTTTGGCTGAAGTCTGAAGCTGTCTTGGCTGCTGTA
GAGGCAGAGAAATTAGCTGCTAATGCAATCTGGGCTGAATTTGTTAGTAG
CAAGACAAAGGTCCTTCAGCGCTAATGCTATCTGGTGTGATTTCAATCTC
TTCAAGGCTTTGTTGTAGAGTACTCTTTTCCAAACCTCATTTGTTGGG
TATTGTTAACTTTTGTCTCCACTTTGTTGGTATTTTACGTTGTTGAGAGAT
ATGGTGTGCTGATCTGTGTTTGTCTATGGGTGCTGATCAATGATCTGCTGT
AGACCAACCATCTCAAGGGTGTGGTAACTGTATGATTTGATTTGTCCT
GTTTCTATATTTCTGTTTGTGCTACTACATCGGGCTCCAATTCCTTATGTC
GTTTGTCTGAAAATTTCCATTTGAGAGTCAAGTCTAAGGCTATGCTCTAT
TGCTACAGCTGACTAATTTGGTTGTGGGTTCTGATACGTTTCTCACTC
CATTTATTACTGGTGTCTATTAACATCTCATACGTTTACGTTTCTCAGGGC
TGTTTTGGTCTTCAATGTTCTTATGTTTGTGTTTGTGTTTCCAGAAACTAA
GGTTTGTAGCTTTGGAAAGATCAACACCACTGAAGAGAGGTTGTTCTAC
CATGAAGCTTCTCCCTCATGGTTTCCCACTCACTGAAGAAGGTCCTCAATCT
CACGCTGAAGAAATATGCTCACGATATGAGCCATTTGTATCAAGAGAAATGTT

CAGCACCAGTAATA

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YDR343C, 570 aa (SEQ ID NO 122)

MSDDAALAEQTPVEHLASVDSASHSLSTPSNKAERDEIKAYGESEHEP
 VVELPKRPASAVYTVSIMCIATFAGFVGMDTGTISGFINQDPIFRFG
 MKHDGNYLSKVRITGLVIFINIGCAIGIILSLGDMYGRKVLIVV
 VYIYIGIIQIASINKWYQFPIGRITISGLGVGIAVLSPMLISEVSPKHL
 RGVIVSCYQLMTTACIFLEGYCNFGRKNYSNVQMRVPLICFPMALFMI
 GMLFVPESPRYLAIEVKRIEAKRSIAVSKRVAVDDPSVLAIEVAULAGV
 EAEVLAGNASWGELEFSSKTKVQRLIMGAMIOSILOLTDNRYFYVYDTI
 FKAVGLSDSFERSIVLGIWVFASTFGLIVERYGRRTCLLMGAASPTAC
 MVVVASVGTRLMPNGDDQPSKSGAGNCMLVFACFYFCFATWAPLPYV
 VVSEFPPLRVKSKAMSIAATAMWMLGFLIEFPPTFITAINTFYGYVFMG
 CLVEFPFVLIVPETERKGLTLEEVNTWMEGVLPMKSAWVPPSRBGANY
 DAEMAHDKPLVKRMFSTK

YGR192C, 1499 bp, CDS: 501-1499 (SEQ ID NO 183)

ACAGTTTATTCCTGGCATCCACTAAATATATGAGCCCGCTTTTAAAGC
 TGGCATCCGAAAAAAGAAATCCACGACACAAATATGTCTTCA
 CCAACATCATTCATAGGTCCATCTCTTAGCCCACTACAGAGAACAG
 GGGCACAAACAGGCAAAAAAGGGACAACTCAATGAGTGAAGCAACG
 TGGCGAGTAATGATGACACAAGGCAATGACCCAGCATGATCTAT
 CTCATTTCTTACACTTCTATTAACCTTCCTCTCTCTGATTTGGAAA
 AGCTGAAAAAAGGTTGAACAGCTCCCGAAATATTCCTCCATCTTG
 ACTAATAGTATATTAAGAGGTAGTATGATGTAATTCGTGAATCT
 ATTCTTAAACTCTTAATTTCTACTTTTATTAAGTTAGTCTTTTATAGT
 TTTTAAACACAAAGAACTTATGTTTGAATTAACACACATAAACAA
 ATGTTAGAGTGTCTATTAACGGTTTCGTAAGATCGTATGATGTGAT
 GAGAAATTCCTTGTCTAGACCAACGTCGATTCATGTTCAAGTACATCC
 CATCTTACCAACGACTACGCTGCTTCAATGTTCAAGCATCATCTT
 CACGGTAGATACCGTGGTGAAGTTTCCACGATGACAAAGCATCATCT
 CATGTGTAGAGAAATGCTTACTTACCAAGAAAGAACACCAAGTATTC
 CATGGGTTCTTCCAGGTTCACAAAGACATTTGACGTGTGCCAAGGT
 AAGGAATTAGACATGCTCAAAAGACATTTGACGTGTGCCAAGGT
 TGTATATACGCTCCATCTTCACCGCCCAATGTTGTCATGGGTGTTA
 ACGAAGAAAATATACATTTCTAATGAAATGTTTCCAAACGCTTCTGT
 ACCACCAACTGTTGGTCCATTTGGCCAAAGTTATCAAGCTCTTCGG
 TATTTGAAGAGTTTGTATGACCACTGTCCACTTTGACGTGACTCCAA
 AGACTGTGACGGTCCATCCACCAAGGACTGAGAGGTGTGAACCGCT
 TCGGTATACATCATCCATCTCCACCGGTGCTGCTAAGGCTGTGGTAA
 GGTCTTGCCAGAAATTTGCAAGGTAGTTGACGGTATGAGCTTTCAGATCC
 CACCGTGCATGTCTCCGTGTGTTGACTGACTGTCAAGTTGAACAAGAA
 AACACCTAGCATGAATCAAGAGGTGTTTAAGGTGCGCTGCTAAGTTAA
 GTTGAAGAGGTGTTTGGGTTCACCGAAGACGCTGTTGTCTCTGACT
 TCTGGGTGACTCTCATCTCTCCATCTTGCATCTGCTCGCTGTATCCAA
 TTGTCTCCAAAGTTGTGTCAAGTTGTGCTCTGCTGACGACAACGAATCGG
 TTACTCTACCAAGAGTTGTGACTTGTGTTGAACAGCTTGCCAAAGCTTAA

YGR192C, 332 aa (SEQ ID NO 184)

MVRVAINFGRIIGRLVNRIALSPNVEVVALNDPFIINDYAAMFKYDST
 HGRVAGEVSHDKHIIIDGKIATYQERDPANLPMGSSNDIAIDSTGVF
 KELDTAQOHIDAGAKKVVITAPBSTAPMFVGVNEEYKTSIDLKIVSNASG
 TTNCLAPLAKYINDAFGLEGLMTYHSLATATQKTDGPRSHKMDRGRTA
 SGNLIIPSTGAIAVKGKVLPELOGKLGMAFRVPTVDVSVVDLVTKLKE
 TTYDEIKRVVXAAABGKLGVLGYTEDAVVSDPLGSHSSIFPAASGID
 LSPKFKVLVSWDNEYGYSTRVVDLVEHVAKA

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YOR374W, 2060 bp, CDS: 501-2060 (SEQ ID NO 373)

CGACCCCTGTGGTAAATGACATCCCGCCCACTGCGCAAGATCTGTAA
 CCCCATTAATCTATACCGGTACGAGTACTAAAAATGATATTAAGTAAA
 TGTATGTAAACAATTTACCGGTTTGTGTAACATTAATTCATTCATTTT
 TTGATCCCTTATGATCCCGCCGAGCGTATGATCCCTGTCACATTTTGT
 TTTGCTGTGATATCCCGCCGAGCGTATGATCCCTGTCACATTTTGT
 ATCCGGGACTTCCGTCACAGTATCTTTTCTTCCATCCACAGATAT
 GGAATAATGAGGGCGGGGTATGATGATGAGGAGGAAATTTGTAT
 GAATAATGAAATTTCCGGGTATATTAATGAGGGGGGTTTGGGTGACA
 GAAATATGAACTCTCTTCTTCAAAAATTTGGGTGTATGATGATGAA
 ATTGAATGAACTCTCTTCTTCAAAAATTTGGGTGTATGATGATGAA
 GTATCTGGAAAAACAACAAGAAATCTCAATAACAATAAATAAAGAA
 ATCTTACGTAGTACTAGCTGTCTTAAAGCGTCTGATCTTCCATTGG
 AGATCTCAATTTAGATATTTTCCACCTTCTCTTGAAGTGGCTATCA
 AGAGGCCAAATGGGTGAAATGAGCAACCAAGGGGTGTGTATCAAC
 AACAGTTTGTCTCTTCAACAGAACAGACCTTCGAAGCAATTAACCC
 TTCCACGAGAGAAATATGTATATTAATGAAGATGAGAGACGATG
 TTCCAGAGGCCGTGACAGGCCCGACCGCTCTCTTAATGGGTCTTGG
 TGGAAAGGCCGTGACAGGCCGTAAGGCTTTGTACAGTTAGCCGA
 AAGGATTCAGCCCTATTCACAGGGGTAAAGGCTTTGTACAGTTAGCA
 ATTATATGAACAGGACAAGATTCATTCCTTCCATGAGACTTTGGAAT
 ACGTAAAGCTATCTCTTCTCGAGAGGAGATTTGATTTAGTATCAAC
 TATTTGAATCTTCTGCTGCTTCTTCTTCACTAAGACAGCTTTGGGTG
 TGTACTGTAGTAACCAATTTTCTTCACTAAGACAGCTTTGGGTG
 TTTGTGGGCAATTTATTCCTGGAATTTCCACTGTGTATGGGCTGG
 AAGATTCCTCTGCTTGTGTACCGGTAAACCGTGTGTAAGAATCG
 CGAATCCACCCCATTTGTCAGGTGTAACCGTGTGTGTAAGAATCG
 AAGATTCCTCTGCTTGTGTACCGGTAAACCGTGTGTGTAAGAATCG
 CGGTATTTCCACTGTGTGTATCAATTTGATTCGGGTGTTGGTAAAT
 GTGGGTAGGCGCATTAACAACATCAAAATCAAAAGTGTGCTTAC
 AGGTTCACCGGCTACGGGTAGACATTTTACCAATCCGACCGGCAAG
 TGAATAAAGTACTTGGAGGTGGGTGATTAATCACCAACATTTGCTTC
 GCGGACCGCGAGTTGAAAAAAGCCGTGCAAAACATTAATCTGTATCTA
 CTAAATCTGTGTGATCTTGTGTGCGGTTCAGAGGTGTATTTGAAG
 AATCATTTTACGACAAATTCATTAAGAGTTCAAAGCCGCTTGTGAATC
 ATCAAGGTGGCGACCATTCGATGATTAATCTTCTTCCAGGTGACAAAC
 CTCTCAATTCGACATTAACAATAATCTGAATACGTTGATAGTGTAGA
 ATGAAGGTGCTATCTTGTATTAACCGGTGTGAAGATTTAGTACAAAGGT
 TACTCATTTAAGCCAACTGTCTTGGTGTGACGTTAAGGAACATGAAAT
 TGTCAAAAGAGAAATCTTGGCCCTGTGTCTACTGTAAACCAATTCAAAT
 CTGCCGAGGAATCATTAACATGGGCAAGATCTGTGAATCGGGTGTGCT
 GCTGTATTCACACCTTATATTAATTAATACCGCTTAATAAGGCTGTATG
 AGTTAATCGGGGTAGGCTGGAATTAACATTAATTAACGATTTCCACACG
 CAGTTCTTGTGGGTGTGATGCAATGCAATGTGTGGGCAAGGAATGTCT
 GTTATGCTTTTCAAAAACATCTTCAAGTTAAAGCGGTCTGTCGCAAAAT
 GGACGAGTAA

YOR374W, 519 aa (SEQ ID NO 374)

MFSRSTLCKTSSASISGRLOLRYSFLPMTVPYIKLPMLEVEQPTGFLIN
 NKFVPSKQNTKEVINPSTBEELCHIEGRHEDVEAQAQADRAFSNGSM
 NKIDPIDRGALVRLAELIEQDDVLAISLETLDNGKALSSSRGVDVLTIN
 YKSSAGFADKIDGRMIDGRTHFSYTRQPLVGGOIIPMNFPLMMAMW
 KTAAPALVNTVTLKTAESTPLSALVSKYIPQAGIPEGVINIUSGFGKI
 VGEATLNNPKIKVAFPGSTRATGHIYQSAAGAKLKVTLLEGKSPNIYF
 ABAELKAVONIIIGIYNSGEVCCASRVVEESLYDKFIEFEFAASIS
 IKVGDPEDESTFGAQTQSQMLNKILKYVDIGKNEGATLITGGERLGSIG
 YFIKPIYFGDKEDMRIVKEIFGPVTVTYFKSADVETINMANDEYGLA
 AGIHTSNINTALKAVDVNAQVINTVNDPHHAVPFGGFNAGSGLREWS
 VDALQNVLTQKAVAPAKLDE

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NAHLETVKV

YLR110C, 902 bp, CDS: 501-902 (SEQ ID NO 275)
 TATTTGGGCTGATTTCCGTTTGGGATATCTTGGCCGCGCCCTCTC
 AAAATCTCCGACAAAGTCCCAAGAAAGCGGGAAGAAATTAACGCGCA
 AAAAATAAATAAAGCAATCTCGAAGCGGTGGTGAAGCCCTCGA
 TTATCCCTACAAATTTCTCAGAGTAAATAAACGTTTGGTGGAA
 TTCCCATTTGCGGCGACCTACGCGGTATCTTGGCAACAATCTTGG
 GATTAATGCAAAATTTTGCATATTCGTGCAATATTCGATTAATGG
 AGTACTTCTCCACATACGCGCAAAAGAAATGTGAATAATTTGCAT
 CCTTGGCCCTGTCAGATATAAGTGGCATGCTGTGATTAATCTTCT
 TTCCATCCCTCAATTTCTTAATTAATTTCTTCTCTTAATCTTCTTA
 ACATACCAAGAAATTAATCTCTGCTATTCGTTAAACATATATCAATA
 ATGCAATTTTCTAATCTGCTGCTTATGCGCGCTGCGCGCTGCTGCT
 TGCCGCTGTAAGTTACCACTGCTATCTGCAAGCAAGATCTACACTT
 TGCTACCACTACTCTTCTTGAAGACCAAGTCTGTTGAACGTTACCTCA
 CCAAGTTTGTGTTCCACCGCTACCGTACCGTGTGATGATGATTAATCTCA
 ATACACCACTGTGTGCGCATTTGACACTGAAGCCCAAGAAAGGATCTT
 CTACGCTGCTCCAGTTACCTTACTGATGAGCTCCAAAGACACCACTCT
 GCTGCTCCACTACTCTGCTGCTGCTTACAGCTGCTGCTGCTGCTGAGGC
 TTTGCGAGCTGCTGCTGCTTGTGTGGCTGTGCGCTGCTTGTGTGTGT
 AA

YLR110C, 133 aa (SEQ ID NO 276)

MOFSTVSIANAIVAAVSAANVTATVTSQSESTLVLTITSCEDHVCSEVTS
 PALVSTATVTVVDVITVYTTWCPLTEAPKNGTSPATVTSLEAPNMTTS
 AAPHSVTSTYGAAXKALPAAGALLAGAAALL

YLR109W, 1031 bp, CDS: 501-1031 (SEQ ID NO 273)

TGCTCTATTGTAATCAAGAAAGAAACCTTAATCATTCGCGCTCCCTGTG
 TGCGCTCTCGGAAAAACCGGCTCTGACGCTGACGTAAGAAATTTCCGACAT
 GGTTCATCGGACAGAAAAATTAATTCGACATGCGTAATATTTCTTCTCC
 GTTAAGGTAGTGAAGCGGATTTTCTGATTTGTAATTAATATCATCTTTTTC
 TCTGGCCAAAAAGCTCAGTATTTGTTGTAATGAGTGAATATCATCTTTTTC
 ATTTTCTTCTGATCATCTTTCTTTTCCACACCCCTCCGCGACGCT
 ATTACATATTTGTGAGAGTTAAATGAATAAATAAGGCTGAAAAATTA
 AGACGAGATGTAAAGGAAAGCAATTAACGAAACATTAATTAAGAGCA
 CAATTTCTCTCCCTTCCCAATTTGATATACCGTTCTTTTAAGAGCA
 ATTTCAACAACAGAAACAACAAGTACTACCAATTAACCAACAACAAAC
 ATGCTCTACTTGAATTAACAAGAAATTTCCAGCTGCGGACCTACAAATTC
 ATACATTTGCTATCAAGCCAAAGTATGACAGTGAATCTGTGAATATGTC
 CACAAACGTTGAATGTCTCAATTAATTTCTGAAAAAGAGGTTATC
 ATTACCGGCTGCTCCAGCTGCTTCTCCCAACCTGATCTGTCAGCCATAT
 TTTACGTTTACATCACTACTTGATGAATTAATTAAGAAAAAGGAGTTG
 ACCAAGTATGCTGTTACTGTTGACACACCGCTTCCGTAACCAAGCTG
 GCTTAAGATTTAGTGTTAAGACACACACATCAAGTTTGGCTCGA
 CCGAGAGTGTGCTTACCAAAATCCATTTGTTGTAATTAAGCCGTGCTG
 ACCGCTGTTTACTGAGTGTGATGAGGCAATGCTTGTGAAGAAAGGATTC
 GTTACTTACCGCTGCAAGAAACCAACCCAGGATCCGATGTGACCGTTTC
 CTCAGTCAAGAGTCTTGCGCTCATTTTGTAG

YLR109W, 176 aa (SEQ ID NO 274)

MSDLNKKFPADYKFOYIAISQDADSESKMPQVTEWSKLISEMKVI
 ITGAPAAISPTCTVSHIPGIVINYLDELVEKEVDIVIVITVDNPPANDAM
 AKSLGVKIDTTHIKFASDPGCAFTKSIPELAVDGVTVWSGRMANVVEGSI
 VTYAAKEINPGIDVTVSVSVSLAHL

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YBL081W, 1607 bp, CDS: 501-1607 (SEQ ID NO 29)

TTGTGCAACAATTTTGGGATGCTTCTGCTGCTGACGACCTGTATTTAC
 CTCTCTAGCTCATGCTTCCAGGCTCCAGCTTAATTTTTCAAATTTTTC
 CTTCGCTGCGAAAGTTGAGTCTGCGAATAATTTGCAAAATTTTTCAC
 TAGATATTAAAGACTATATACATGCAATTAAGATGCCAGACAGAGAT
 AGGCAATCAGATTAGTATGACAGACATCTCAATATGTCAGAAAGCAAA
 GCGAGATGAAAAAAGAAATCCGTTTCCAGCTTCTTCTTCTTCCCA
 TTCCGTTTTTCTGATCTTTTCTTCTCATGCTGCGACCTTAAGAAAGAGG
 TACCTTCCATCTTCTGCTTAATTTTGTATGATGCACTTTTGTGATTTTGT
 ATTATTAATTTGTTACTATATTAATTAATTAATTTGATTTGCTTTTGT
 AATTAATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT
 ATGCAAGGCGCAGATATACAGATTCGTTTCTTTTCTGCAAGACAGACAT
 GGAATTAATCTTCTGCTTCAATGAGCTTCCACAGCTGCACTTACAC
 CCCCATTACATATCAATGAATAATTAACAACAAGTGTGATTTACTATTA
 CCAACACATATACAGAGTGAATTAACCAACATTAACCAAGCTGCTAC
 GAACACACATATCAATTTCCATTCGCTGCTGCTGCTGCTGCTGCTGCT
 AATCCATTAAACAGATCTATTTCCATTCGCTGCTGCTGCTGCTGCTGCT
 AACAGAGCTATATGACGATCCATATATGATATCCAAAAAGAAACACAG
 AATTAAGCGCTTAACAATTAATTTGAACGCAAAATTAACAGCAATATCC
 ACTATATGCTCAATTCATATGTTACTGACATCTGAAAGCAAAACGTA
 CCACTGTACTCAATATGACAGTATGCTGACATCTGAAAGCAAAACGTA
 CAACATCAACAACAACAACAACAACAAGACAGACAAACAACAACATCTT
 ACACAGAGAGGAGTCTCCAGAGTACTTCACTGACCTGACCTGCTTCC
 TCGTTGACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
 CTTCGATATACATTTTGGCTTCACTTGGAGCTTTCACAAATTTATCTGT
 CGGTATCATCAAAACATCTATGACACACCAACCAACCAACGACATCTG
 ACATCCGCGGATTTATCAATGATTTACCGTGGGCTCCACGCTCCAGTTC
 GCTATCTCGATCTTACATCTTCCACCAAGCTATGCTTATTTGGACCAAC
 GCCAACCCCTGCTCATCTCTCCACACATCTGATGCTTATTTGGACCAAC
 ATTAACCCACCGCAACATTCACCATTCCTGACGCAAGGAGAGATTTTC
 GACGCGACAGTGAACATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG
 CTTCCTTTAGATGAGGAGCTTCAACACATGATCTTCTTCTTCTTCTGAA
 CCAGCATCATCAAGACCTTTGGCATTTTGAATTAATGATGATGAGCGTTTG
 GAGTTGA

YBL081W, 368 aa (SEQ ID NO 30)

MPGQIISPLSQNEDMDKYLLEYRSIKLLHQSSNSFOSHAPSHQSNYH
 PHVHMKYNTGSIYYNNNNNSVPHNQAGLQSTNRSIPSPYGAYNQ
 NRVADVPYMATYQKHHKPSANNNLINQKXKQYPOYSNPVTTAHLKQYTP
 OLVNSNVNAHNNNNNNNNNNNNNNNNNNNNLNNNNNNNNNNNNNNNNNN
 SLTSTSSSSSPYNGSTPEYLLPSTAASTNLSSSSSSNNNNNNNNNNNN
 TSADLINDLPVGPSTSLISDLHSPPTVFLPASQILNMSSTSSISGTV
 INPPOHSPSPQREDPSTPAVNINSSASLLMDSLSLQWGSNHNWVSSSSQ
 PASRPFGIWNTDMSWVS

YDR366C, 899 bp, CDS: 501-899 (SEQ ID NO 125)

CTGTGCTATTTGGGCTACTTGTAGTGCATTAATTTCCATCAATATTTAGCA
 GTCATCTTCCAGGTGAACCATTTGCTGTGTAACCATTAAGTAAATAAACA
 AGTGAATAATGATATGATGTATTAAGTACAGATTTGCGAATAATTAACA
 GCAAGTTTGGCTTAATATCAATCAAGCTTGTGAAATTAACGATATG
 GTAAATACCGACCAATATGATATCAATTAAGACCACTGATTTGTTAAGA
 ACCGTGAACAATGTCTAAATTAACATCAAGTATGAGCGGATTAACCC
 TGAATAATACCTAAGACATCTCAATGCAAGTATGAGCGGATTAACCC
 AAAAAAGACTATGAAAAAATTAATTTTGAAGAACAGTGTGTAATAATG
 TGCTTCTGCTGATCTTCAAGTAAACAAATTTTAATGCTTTGCTGCG
 GAACACTACTTTTGAAGGTTAGAAGAGATGATCTCAATTAAGGTTTA

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ATTTCATACAAAGGCTTCCTTCTACAGCGTGTGAATTCGACTGATGAACAG
 CGCCCTTGTTCAAAGTCTGATGAATCCCGTGTATGGCAACGGACGAG
 TPAAGCAAGTTTCTATGATTTATACAGCGTTTACGTGCGAGTACGCA
 TTAATACGACTGCGCGCTGCCACTGCCATTAATCAGTAATATAGTGAAC
 TATACGCGTGGGACGATGTTCCGATGTTCCAGAAATGTTTTTGTACA
 GGCAGAGAAACAGATTTTCAGTACTGTGCTTCGGGTGATCCCGATCTCA
 AGTTATTCACAATAGTATCATATTCCTCCCGTAAACCTTCGCTCAACTCA
 AGTCATTCGACCTTCAATTTTGGAGTGGGAATGACATGATACGATAC
 TACCGCTGAACAGAAATGACATTGACGCTTACATAGACACAGATATAC
 CCAACTGCTCTTATTA

YB050C, 338 aa (SEQ ID NO 44)

MTLSNCDSLNLFQDPPEEESKFEVAVRTIAMPNDKPYPPAANGTYC
 LKIKISLNAQWKINKRMCMIPAVKKNFDFEQRSLINLNLWFIYF
 INCSKNYNKNKHVSSNNTVKIENVLPLOKHKVNDQLENLFWRS
 WFKARKRDINGKPREHIKFENDVEQCIIDENHFIQRLPSTRLNSTEQ
 RPSKSELDPCIGNAASKRSFYDINSVVASDAITTTAAATLISNSGD
 YQGHDRDVPBNVLLQGETDFSSVLKRVSDLKLSNISHSPVKRSTIS
 SHSTFIESETDPTDPAETENDIDAYIDTSTPNLLT

YEL071W, 1991 bp, CDS: 501-1991 (SEQ ID NO 143)

TAGCTGACCTGTCAGATTAATCAGCTTCACAGTACTTCCCTTCCG
 AAGATCTACCCAAATGCTGAGACCTTGATATATACAGATATGCTTC
 GTCCGACTTGCAATTTTAAATTTCTAAGTCTTCTTAAAGAAC
 TAAATGTCAAGAAACACAAATTTGCTCAATGTCACACAGAGGCG
 GCATTTATGTTTTTCAATTTTTTTTTTTTTTGTGCGTGAATTAAGCGG
 GATATGTGCCACAGTCATTAAGATGACCATTTGACAGCTTATGCTTC
 GGAATAATTTCCAGCGAGTGAACCACTTGCACAGTTGTCACGCCCA
 AATCTAATCTACGGCGGAACTGAAGGTTGTGATATATATATGCTCA
 TATTTTATATATACGTGACGAGGAGAACAGGGTCCAAATGCTCCCAA
 TATTTTATTTTATGATTCAGTCAAGCTTAAAGACAGCATATTAAGATT
 ATGACGGCGCACATCTCTGTGCTCAGTTAATCCGAGGCAATCCCTAA
 AGTCAAGAAACCCAAATTTCAAGTCTCGATTCGAACTGAAAGTTGGCT
 ACTTGTGTCGATTTGTCAATAGTAAATCTTAACTCTCAAGCTCA
 GAAAGCTTGTCCGTTTACAGAGACTGATGAAATAATATAGAGCCA
 GTCCATTTAATTTCTTCCCAAATCCCACTGATTAAGTGTCAAGATTA
 TGAATPACTGTACGATTAATAAAGTTGCGAGTATGACACAAGTGTATAC
 ACCGACTGTGCGAGCTCTGTCCGCTATTGATGATGATTTCTCTTC
 TCTAAGAAATATGAACAAGTCAAGATTTTGTATCTCAGTTAGCGGACTT
 TCAAGTGTACCGGGTGTGTTATGGGTATGGCATATGCAATTTTATAC
 GACCATGACCATATCTTCCATGTGATCTGCTTCTAGAAAACACTGTCA
 AGTGGCGGTGTAGTTTCAACAATATGCAAGGTGTGAATCTTTTAAGT
 ATGGGCTCTACACGGTATGTTTGGGTGTGAAGTGTGTACCTTCCAAC
 GGTGATTTATACGCAATATCAATGCCCTAAGGAGACAAATATCTGTAA
 TGCATTGAACAATTAATTCATCGGTGACAGAGGTACTATCGGTGTGTTA
 CTGGTATTCATGATTTGACAGCAAGCCAAAGCCCTGTGATCCGTTA
 TTTTGTGTATGTGAATTCGATACCTTCAAGAAATTAATTTGTCAAGCG
 TAAAATGTGAATTAATCGAATTTTATCTGCTTTGATATCATGACGCTG
 GCTCCATGTGATGTACATAGATTAATCTTGAAGGACTTGCTTCTCCCTG
 GAGACCAACACACACTTTTATGTTCTTATTTGAAGCTCAGGGTCCATAA
 GAGACACGACGATGAGAACTGACTGCTTCTTCCAAAGCATACCAAGAT
 CTAAATTAATTTGAGAGGTATGATGCTTAAGACAGCTGTATTTCTTAAG
 AGACTTTGACCTTGAGAAATCTGTTCACACAGCTGTATTTCTTAAGG
 TGGTATACAGTATGATCATCTCACTTCAATTAAGATTTATATTTCCG
 TATCTGCGGTGTGACGAGATTAACGACGCGGTGTGATTTGATGAT
 GCACCAAAACCAAGTTTAAATCATGTGTGTATGTGATGCTGCTGACGG

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AAACATCCATTTAAATATCGCGGTAAAGAAATTTACGAAACAGATTGAGG
 ACTTACTAGAACCATTTGTTATGAAATATATTCATCAAGAAAGCTTCC
 ATCAGCTGAGCAGTGGGATTCGGTTTCCATTAAGAAAGTATGATACATA
 CACGCAAGTGAATTAATGAATATGATTTAAGAAAGATATCAAAAAATCACT
 ACGATCCAAATGGAATCTTAAACCATACAGTACATTTGA

YEL071W, 496 aa (SEQ ID NO 144)

MTAAHVLAQTLAEYPRVKRNPVKVDSEDLAFVRSILSNDELINSQAP
 EELASNDQMKRYRQSNLILPNSDTKVSIMKYCNDKILAVPQGN
 TDLVGASVPVDFEVLSTLNMNRYRDPVSGFTKCDAGVYMRDHOQLH
 DHDHIFPLDLPSRNNQVGVSTNAGLNFIRYGLSHGALGLEVLN
 GELISINILRKDNTGYDLKQFLGAGTIGVTGVSILVAALAKPRALNAV
 FPGIENFDVYQKLFVAKSELSELSAFEFMDRGSIECTIEYLDKLPPL
 ENQHFVYLIEGSSNNRHXDEKTLAPLKQDTDSKLISEGMAKRAQD
 RLMTWRKSVPTACNSYGMKYDMSLQDKDLYSAATVERLINAAGLIGD
 APRVVKSCGVGHVGDNIHLNIAVREPTKQIEDLLEFVYEVYIAASKGS
 ISAHEGIGFHKKGLHYTRSDIEIRFMDIKNHYDPNGILNPKYK1

YDR133C, 836 bp, CDS: 501-836 (SEQ ID NO 95)

GTGCAGAGGGGATCAACGGCCCTTCACAGAAACCGCGCAGAAATTTT
 TCTGCTGTTTGTATTTTTTTTCTCTGTACTATCTCATCTTCTCTTTT
 CTAACTATTTTTTTTGCATTTTTTTTGTGTACACTTCCACAAATATG
 GATGCTTATGATCTCGAAGATATTAACCGTTGCTGAGATCTGTGTT
 GTTCTTCAATGACCTTCTCTGTGACACTCTCTTTTATTAATTTTCA
 TAGAATTAATAAACAGAGATTAACAACATCTTCTTCTGTTCCGTTAAAA
 TAACTACAAATTAATAATGCAATTCCTACCGTCTACATCTACTCTGACA
 TTGCGCGTGTGCTCCCGCGCTTCACTTACATTAACAATCTACTACTGTCACA
 GAAATCTACCATCTTGTGCTCACTTACATCTTGTGAGAGCAGCATTTG
 TTCTGAACAGTTTCCCGACTTGTGTTTCCACTGCTACCGTCAAGCTTAA
 ATGACGTTATCACTTAATTAACACACTGTGTCAATGCAATGCAACATGAA
 GCACCAAGAAATACCATCTTCTCACTGCTCACTGAAACCAACGCAAAA
 GCGCACTGAATAAGCCCACTTCTCACTGCTCACTGAAACCAACGTTAACT
 CCTACACTGTGCGCTGTGTTAAGCTTGTGCGACGCTCCGCTGCTTGTG
 GCTGTGTGCGCGCTTATGTTGTAATTAATCACTTCTTCTTTAATA
 TATTTTGAATAAATGTTAATCACTTCTTCCGCTACATACAGCTTCCACAA
 AATGCTTTATTTCAATTAATTAAGATATTTCTGTAA

YDR133C, 111 aa (SEQ ID NO 96)

MTLSINTPBGVHCQPLKHQRIPLDQILKSQPKSOLKSOPNVLAIKLIP
 PTLVPLRLCOLPVLQMLVLPVCCMLNLFNIFLEKMLSTPFSIQLPQ
 NPFISINKIEM

YHL021C, 1898 bp, CDS: 501-1898 (SEQ ID NO 193)

GGTAAAGAAATGATCAGGAGCGTTCCTTGGCAACAGACAGCAAGTAC
 GGCAGCAACAGCAAGAGATGGAATTAAGTAAAGCCCTCAGGACAC
 GTGATATGCAAGAGATTAACGAGACATATGAGTCTTTCATGTCAATACC
 ACCAGTATTAATTAATTAAGGAATATATAGTTATTAATTAATTCATAT
 CATATATCATATATCATATATCATATATCTGTATTTGACAGGCCCC
 GCTTCTCCCTTTTGAACATACATATATATATGAGGACCCCTTCACTTTGA
 ATGGCTCAGTAAAGCACTTTCGACCGCTAAGGGGCTCGGGAATACATY
 TCCGGGTTATCTCGAGGAAAGTGTCTATCTATATAGGAGAAAGCCCT
 TCTAGATTCCAATATATCAGGGTAACTCTTCAACACTGCGCAGAACATAT
 TCCAAATTAATAAGAAATAATTAATTAAGAAACCAATTAACCAACAAG
 TCCATAGATCAAAATTAATGAGAGATCTGGAATCCCTTCAAGACTGAC
 ATGCTAAGATCAAAATTAATGAGAGATCTGGAATCCCTTCAAGACTGAC
 CACTACCAAGAGACATCATCTGCGCGACACTGCTGCGCTGCGAATC
 GGGGACATATCATCAAAACATTAATTTCAATTAAGATTTCTACGAATTAAG

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YLR311C, 848 bp, CDS: 501-848 (SEQ ID NO 283)

ACAAAGACAGCTTATTTTATTTATGCTATACACAAAGCTCGATATGAAA
GAGCGTTGGCACANAGAAATTTTAAACAAATTAACGAGAAAGTTAAACGTT
ACACCTATTTTTCACAGAAATTTTAAATCCGCTACAGAAAGTTAAACGG
TATTCGATTAAGAACAGAAACGCCCTGGAAAAGCTCTTTGTGTACTT
CATATTAATACAGGCAATTTTCTCACAATTTAAAGSTATTTCATGAC
TTCTTCCCAAAGGAAACATGTTGCTGGGATTCGAAATTCAGTTGCC
GACAGCTTGTTTCAATGATCAATGAAACATTCCTCGAGTTTTCAGTTAAG
GTTCCGAAGATACCACTGGTTTGAAGACAGCTGAAATCCGTTGCGATT
GTAATTTACAGACTTTCGAGATGTATTAACGATGTCCAGATACAGAAA
AAATTTATTTTAAAGTCAACACTATACATTCAAATCCACAGATGACAGA
ATCGAAATTTCAAAAGAAACAAAAAAGACATGCTTGTAGGAGTGCATCA
TATTCCTCCCTTAAATTTTTCACCTTACTCTCTTTTATTTTATTTAGAAA
TAGAAAAGGTGACATCTCTCTCTCTCTCTCTCTATCTGATCTCTAAGG
TTTTATTTACTTTCATTAACGATACCTATTCATCTCTTTTCTCTTTTTCG
TTTTTGTATTCCTTTTATTTTATCTAGTTAGATTCAATACATACATTAATTA
ATTTTCTCGAAGCTTTTATGAGCTAAATTTTGTGTGCTTATTTGGGACCA
GAAATTAATGTCGACGTACGTACCTCCAGGTTATTATGTAATTCGCTTAA

YLR311C, 115 aa (SEQ ID NO 284)
MKLTKEKNDCLGVSTIPLNFTYLTFLRLRIEKVHLSSTLSSTLR
FYFHHVCYSTLTFPCVAVPFYSVAFILLYHLIRSFYENILLLYGA
ENSHRQSPFGYVIR

YMR107W, 848 bp, CDS: 501-848 (Seq ID NO 309)
AGACGAAATTAAGTAAAGGCTTACATACGCGCTCCACTGATGTGCTCGTA
GTCAATGATTTACGATTAACCTACATCAATCAATGAGAGCGGCGTACCCC
AACCAGAAAGATGATCTTCCCTGCGCTGTTCGCAAAACCCCATACATGCGC
ATCTGCGCTTCGCGAGGGGGGTTGATGACAACTAGCGCCCTCCCTTAAT
ATTAAGCCCTCCACAGGCACAAATTAGCAATTTCTCGGAAAGTAAACC
AGTCAGTTTGCGCTTTTATGACATGGGTATTAAGGTATTAAGTGAAGTA
GTGTGGACAGAAATCAGGAGAGATTAAGAGGAGGAGGGGGGTATGATGT
GCGATTAACAGCTCTGTGCTATACACCCCATATCTTGTATGTAGTATGT
ATTAATTAGAGGCTCCCTCCATATGCAATCTCATTAATTTTATTTTGT
AGCCCTTCTGTACCAAGTAAATTAATAACCACTTAATGAGATATCAAT
ATGGGTATGTTTTGGAGACGATCGATGATTAACCAAGGAAAGACACGC
AGATCCAATGTATTATGAGAGAAACCATTAACAACAAGAAACAGTAA
CGCAGGATTTATTTGAAAGAGATCCGCTAACCTAGAGCACATCAGCA
GAGAACTTCACAGACATGAGAAAGATCTTCCATAGGATCAACAGCAATTC
CGATTTGTAGGACGTTTATGAAAGAGGAAATTTACCGGACAGATTAAGAAATTC
CAAGAATTTGACATCTTAAACATGCGTCAAGGTGACGTTTATTAAGACTT
TACGAAAGTTTGTAGAGGGGGGAAACCCGACAAATTAAAGTAAATGATTA

YNR107W, 115 aa (SEQ ID NO 310)
MGSFMDAFAVYDKKKHADPSTYGGNNHNTGSKQVMEFSKEYRQPRTHQQ
ENLQSRSSISGQSDSDVEDVKGRLPAEVEIPKAVDISNNSQGEFLRL
YESLRGGEPPNKKVNR

YK1066W, 944 bp, CDS: 501-944 (SEQ ID NO 243)
GAAAACATCATTAATATCATCCCTGGTAAATGCTATGCTAAACAGAAA
GAACTTTTATTCGGCTTAAACCAAGATGTGTCACAGGGCTTATATCT
CAATCTATCTCGTGTAAACAAAGTTTCAAACTBATTGTTCTATTAA
ATTAGTTTAAAGCGATGATAATTATCTAGAGCAACATTACGACGACAT
TTGGTAAACCATTTTCCCAAGATGTATCTTTATGAATCTGTGCC
ATTGTGGCAACGGTCTGGAGGAAATATGTGTATGACCAAGAAAGAC
TATTTCTTGAGTACTAATCTTTCGACAGTCCACAGTACCATTTAGAG

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GNGATTTTGGGATTATGACCTAGGCGAAGAAAGTCCTGTCACGGCAGTATTCCT
 GTTGATAGCGCGTGAACGTGGAATTCATTTTGGGTGTAAAGAAAGAAAGATT
 AGTTAATTTGGGAATTATTCAGCAAGTGGATTTTATGATGCAATACATTT
 ATGGCATGGGAGGTGACATATGAGCGCTTTTTTTTCTCCTCTTTGGGACG
 CTCATATCATGTTTCCCTCATCTAGCTATGATATATATGAAATTTTATGAGAG
 GAGCAGCAATTAATATATATATATATATACCATTTATGTTGTCTACCTTATATAC
 GAATTTATATATCTTATATGAGCGCTTCAAGAGCGCTGATGATCAAAATGCTTT
 TTGGGCGCCAGGAAATGCGCACACTTCTCTCTCTTCCGACATTTATAT
 GTATCATGTCAAAATATACAGCTTGGGCAAGGTCAATTCACATGCGGCAGACG
 TACGATGTTCAATACGGTTTACAGGATATGCTCTGTATATATCCGAAAGCAT
 GCGTACCGGCATTAATTATAGTATGTTCAATCGCCCTTGACACTATGTAAGGG
 TACACGTAATATAGGCACTTGAATGAGATCTCCCTATTGAATGA

YKL066W, 147 aa (SEQ ID NO 244)
 NAMEGYEELFFFLALGSSHYVPSLANINMIFEGARLYVKKNTTYATLY
 EFLIADASMTEDVKCFMLPVKLPHRLISELSEYLIIEKKLAKVYNNRGST
 YDVHYVSANSVLTSSGMPGIIILGSSSPLDYGVGVQNRQLEMDPLE

YML053C, 1139 bp, CDS: 501-1139 (SEQ ID NO 295)

GAGCGCAGACCTGCTATAGTTTACAATTTTCCGATTTGGGTGGCTAGAGG
CATACATGTTGGCATCGGAGGACACAGCAGCAGTGCAGATGAGAAATAT
GACTTACAGCGTCGAGGAGGACGACCTTGTGAACTTCGATGCCACTA
CCAGACCATCTGCTTTTGTACCTTACACGGTCCATTAGACATTTTA
CTTAATGCAAGATGGCAATTCCTGTTATGACATGTGACCAACAGGATATA
ATTCTTAGAAATCTATGATACACGTATGACATCTGGGATACCTATCATC
TTGGTATCCGATTTTCTCTCCCTTGGCTTCTCTTTTACCTACCTAGCTGA
CTTATATATTTTATTATTTTTCATTTTGTGAAATATATATATAGTTTGG
AAGATACAAATGAGACTCGCAGAAACGAAAGAAAGGCTCTTTTCTTG
GGTGGCTGCTTTTATTTTACATTTAATTTAAGATCATAGCTGGCTGTGA
ATGCTGCTCATCTTTATGAAACATATCTGGTTCACAAACAATTGCA
TTCCGGTAGCAATGCCGCCATACATATATGACAGCGCCATATATGATA
CGATCATGAATGAAAGAAATGACCAATTCGAGTTTGTATACACACT
TTTACCAAGATGGAAGAACAAACGAATCTTATATACAAACACAAACATCA
TTGCGTGGTTCGCGGTGTGCTAATCTTATATATACAAACAAACATCA
TCATACACAAACAACAACAACAACATATATATATATATATATATATAT
AATACACACATATATATGAGCACTTACCAATATATATATATATATATAT
TATGAATATATATATATATGAAACCGGTATGATATGACACACATATGACA
GCCGCTTATCTGACGAATCTGAATTTTATTTTGTGAAACGAAAGTACATC
ATTCATGTTTATTTGGGTACATCATATCGGACATATACAGCACAGCATCG
TACTGAGATGCTCATATATATATACACACAGATATCAATCTTACATCCC
AAGATATATGCTATACAGTACAGCACCGGTATCTGCATAGGCGCGTGAAT
AACACATATATGCTATACGATTTATCATGATATATGATTTTA

YML053c, 212 aa (SEQ ID NO 296)
MLSYEHNTAQTQNNCSGSAALTINSGANDTINAKKRKNDFFEDTHT
FYOSKTRPSTSVSTKSVSGCNTLNNNNNTITINNRRNNNNNNHH
NNSNNATVYNNIIHKKNIEICLPKPVSMHTMNSRLINSEFSETEEM
IAGFGNDNDITGTSTPGSASITQHHYLLPGSIIASQAPETMAALL
INNIANDYMDID

YOR121C, 806 bp, CDS: 501-806 (SEQ ID NO 355)
GTTGACGCTGTTGGGCTACTCTTCGTGGGCTATCTTTCACCAACAAAGA
CATTGCGAATATGTTGACAGCTCTGCACAAATCAGCTGGTTTCCAAAGCA
ATGGTTGCATATGCAAGGCCAAAGGATATAGTTTGTAGAGCTACGAT
ATGGTTGCATACGTTACAGCATGAGCTGAGGCTGTGTTGGTAGAAGC
TAGAGCAATCCGCTATTATTTGCTATTATCCACCAACGCTAACAGCCGTG
GACCAACACCGCTATTATTTGCTATTATCCACCAACGCTAACAGCCGTG

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AGGCCACCAAGATTGTCGAGCAATTTGGCTGACTACTGTATTTGGTGTTCACAA
TACTAATTTATCGAGCTAAGTTTCTTTGGCTTATACACCACTTATCTCTG
GCATCTGGGGATTAGGCTCCCTCATTTTATCAAAATATTTTATGTAATGACGG
CATATTAATCACTGTAATAAAGCCCTCTTTTATATCTAGTCATCATCGGTA
TTTAAACATATTTACGAACAGCTTTAAGAATATACCAATTCGATATACCTT
ATGTTTAATTTATCTACATATTTAGCAATCATACGAGAACACCGCAAAACA
ATTACTGAATATCTTGAAAGGAGCAATTTGGATGTATCAACCCCTTTT
TCGGCTTTCTTCTCGATATGTATATAGTCTTCAAGTCTCAGTAGA
CAAAAGTAATATTTCTCGTTGTTGATTTCGATCGGGATTTACAGATT
TTGCGAGACACAATAACCTCTTTGGAGCTGCCAGCTAATAACACGTGT
CCGGGTGGAACGTTATTTTCTTCGCAATTTCAAGGATAAACCGGTTCCTT
CAATAG

YOR121C, 101 aa (SEQ ID NO 356)
MFNLSTYNHTRNQKLLLEYFERRPIWYVPPFALFYVYIDSKVLSR
QSKYFPVRFDSIGIHRFQDNTISLDVPANNVSLNVIFLENFQDNRFEL
Q

YOL106W, 854 bp, CDS: 501-854 (SEQ ID NO 341)

ATATGGTTTCATCATTTTGGCTCAATTTGTTCTCCATTTGGGTTTACCTTTTGGT
 GTCCAGTTTGGTCGTACTCTGAGGTTTCTTCAGAAAACCTTGCACCCCTTGAAATTT
 TGCCTCTTTTGGCCAAACACTAATTTCTCAGGTGGCTCAGGAATAATTTGGTGT
 GCGCATCTTCTGCTTCTTTTCAATTGATTTACTTTCTTCTGATCTCAATTT
 TAAAGCCGATTTTGGAGCCGATTTTTCAAATTCTCAATTTAATGTAGTGTGTGTG
 TAAACATTTAAAGTCTATAAACCTTTTCTTCTGATGATTTGATATAGATATGGG
 AACATCTTCGCAAGAAGTAGAGCGGCCCAAAAATTTATGCACGTGTAGAAGA
 AAGACGAAGACAGTTAGCTTTTACAAAGTTTGGGAAGCGGTATGTTAAACCC
 TCTGATATATAGCATCTATATAACTTCTGAAATAATGCTCTATTATATCGTGTAT
 TTATATGACGGCTTGGGCATTTCTGGTCTTTACCAAGGTAGTAGAATATTTCC
 ATGCTGAATTTGGCGCAGTATCTTCTGCACCAAGTGTAGATATTTCC
 CAATATTAAATTAATTTCTACTGAGAAATGGGTGGAATTTGAAATTAATTTGTG
 GGATTTCACTCGTATGAATAAGGCTCTAAATTTATAGGTATATACAGAAATGACTA
 GAAGTCTTCCTCGATGATATAGGAATCCCAATATGGAAATCTTATTTCTCT
 ATGTACCAATATATAGATTTATCTCTCATTTCAATATTTCTTCAATTT
 CCTATTACATTTATCGATCCTTTGCGATTTTCAGCTTCTCTAACTCTGGTGAC
 AGCTTCTTCAATAAATCTTATGTCACTATCTATAACACCGTATATGATAATAATA
 TTGA

YOL106W, 117 aa (SEQ ID NO 342)

MLNVRQYRTIETHIFPNINNTEKWNFEIIVGIPSLIKAILGIGNVL
EVLDDIGIPINESIFLCTNITIPHSISYVLSYVIIDPCISASSNFGD
SFYNNLCHYLTPLYIY

>YAL003W, 1487 bp, exon1: 501-580, intron1: 581-946, exon2:
947-1487 (SEQ ID NO 17)

CCGATGGACGTTCTGGAAAAAGAGAAGTAATTAATTACTTCTCAACATAAAATCTCGA
GAAAAACGCAATAGACAGCTCTAABACGTTCCGTCGCTTCTTCTTAGAAGATGTTCTGG
AAGTTTACACAATCCACAATGCGGTTGACATAGTAGAAGAACCATCATCCA
CACACGGCAGCAGGCTTTAATCTTATCTCTGAAATTTTCTTTCGGCGCATTTTCAAC
CAAGAAATTTTCTTAGGGCTCAGAACTCTGAGTGAAGAAGCGCTTTAGAAATTA
AAGCACAACGTAACAATTTGTCACAACACGAGCCTTTGAAGAAAAATTTTTCACATGT
CGCTCTAAATAAATAGTTTAAAGTTTATCATCCCATATATTAGTTAGTTGTTCTTTT
TTCTCTATATCTTTATCTTTTACCTATCTGTCATCTTCAGCATCGAAGAGTCCCA
ACCGAATATATACACACATAATGGCATCCACCGAATCTCCAAGATTGAACATTTGAAC
AATTAAACCGCTCTTTGGGCGACAAGTCATACATGTAAGGGATGTTCCGATTTAGTTTA

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[illegible]

>YAL003W, 206 aa (SEQ ID NO 18)

MASTDFPSKIEITLQOLNASLADKSYIEGTNAVQSDVTVFKAFQSAYPEFSWFNHNIIASAKD
EFDSFPAASAAAEEEDDDVDLFGSDDEADA EAKLKAE RTAA YNAKKA KA KPAKPA AK
SIVTLVDYKPMWDETHLEWNAVAKLEMEGLTWGAHFPIPIGFIGKILQINCVCVVEDDKVUS
LDDIQQDDEEDHQVSTDIAANOKL

>YAL060W, 1649 bp; CDS: 501-1649 (SEQ ID NO 19)

[illegible]

>YAL060W, 382 aa (SEQ ID NO 20)

MRALAYFKKGDHFNIDPRRIQTDDDEVISWCGICGSDLHEYLDGPIFMPKDGCEH
KLSWAALPLANGHEMSGIVSKVGPVKTVKVGDRVVDAASSCADLHCWPHSKFVNSKPC
DACQGSNLCTHAGFVGLGVTSGGFAEQWVYSHHIIIPVKFEIPLDVAALVEPLSVTWH

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AVKISGFKKSSALVLAGAPIGLCTILVLKGGASKIVSEIABERIREIMAKKLVGEVENE
SKHGHSIELRLGTLKSHDGEDYSDSCIGYVTFETSLKALTFKGTATNIAMWGPVPEF
QPMVDVLQEVNMTSGISGVVEAFEEVVAIHNQDIAMEDCKQLTGKQRIEDGEMGEPQE
LMDKESNVKILLTPNNHGEAK

>YB1058W, 1772 bp, CDS: 501-1772 (SEQ ID NO 23)

TTATTTTCATPAGTGCATTTGAACACTTTTCAGCAAACTACGCCAGCCGACGACAGAA
TAAACACACACAAAGAGATCTTTCAGATCTTTCAGGACAGGCGCATACACATAG
GTATATTTGGATGGGATATCAGAGGACATGTGTGAGCTGGATGTTCATCATTTCCAGG
AACTAAGCAACGCTTCGGAAGAGCCGTCACAAAGATTTGTAGTGAACAAACATGCTTC
TGGATTAAGAGAGCGAGCAATGATGAGACATTAATTGAACACACATTTACCTCTT
GTAAATAGTGTATACCATATGATGATTTCAATATATATCTACATCACTATATGTGTT
ACCGCATTAAGAACTTTATGTGTGGGAAATTCATGCAATTAAGAACGCGTACACAC
TAAATAGTGTATGCTTAACTATTTGATTAATATATTAAGAAACGCGTACACAC
AATTATCTCATTTATGATGATGCGGAAATACCTGATGAACCATACAGCATTCATAGG
AATTATACCATATGTGTCATTAACATAGCCGTCATATCTCTGAAATTTGAGATTTAA
CATTGACCAATGTGTGTCATTAACATAGCCGTCATATCTCTGAAATTTGAGATTTAA
ATGAAGCACTAAATTCCTATTTATGCTTCTCAAACGATGACAAAGATTAAGAGAGG
AAGCATTTGGAACAGACACAGAGAGAGAGGCGCTCAAGCAAAAGCCCTTCCACCACT
CTTGCAATTAAGCCATTAATACGAGACGCTGTGTGGTATATGTCCAAACACAGAGCT
CACAAAGTGAACAGGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
GTATAGCCGCTCTGAGAGTGTAACTACCTCAGGTTTATGAGCTTTCCGATGTGTAA
GAGTCAAGCTGATGATGACGATGATGATGATGATGATGATGATGATGATGATGATG
CATCCGCTTGAAGGTTACAGATCTTCAATCTTAATTCATTTGATGATGATGATGATG
AAAAAGCGAGAGAGGAGTGTCAAATGGGCGCTGAAGAGATTCCTGATGATGATGATG
ATGAATGGGTGCGCAATAGTTTATCTGGAAGAGTTTATGATGATGATGATGATGATG
CAGCAGATGAAGTGTGAAGACAACTTCAATGATGATGATGATGATGATGATGATGATG
CAGAGAAATTAAGTATTTGGAAGAGTTTCAATGATGATGATGATGATGATGATGATG
ATGATGATCTCTGGAAGAGTTTATGATGATGATGATGATGATGATGATGATGATGATG
ACCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
AGCTTATTAAGCTCGACGAGAAATCTGGGAGTTTTCAGGCCAGGCCAAAGATCTG
GATCTCTTAATCCCGGTTGAATGTCATCCTGGGAGTTTTCAGGCCAGGCCAAAGATCTG
CTCAGCAACACCATCTCGCAGATGATGATGATGATGATGATGATGATGATGATGATG
CTCAGCAACACCATCTCGCAGATGATGATGATGATGATGATGATGATGATGATGATG
GATACGCAAAATGGCAAAAGAGATTTTTCAGATGATGATGATGATGATGATGATGATG
TGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ATGCTCTTCTCTATCAACATTAAGCAATGATGATGATGATGATGATGATGATGATGATG
TGAATCTCGCTTCTCTGCAAAAGATGCGCATGA

>YB1058W, 423 aa (SEQ ID NO 24)

MAELPDETIQPMALTNVSHNIAVOYLSEFGDLNEMLSYASQTDQKDRREAHMNRQ
QERALKQEAFTSNSSNKAINTHEVGLCPKPSGSGSNEYLRKRGSTSPPTKSSRSGS
GANSRFPSSFMDVMRGQADDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
OMGAEHNGRDEDEHMGANRFTGRGLSTIDADEVVEDNTSQRREKVTREITFW
KEGQVADGRLRYRVDNPANSFYLSELNORAPLKLDDVQGEVEVNVYKLLDSYKAPT
RKLDGFSQGRULGSPITPESSPAEVPKMETPAAEQPMPEDEPKQDSTSIQIRANMCR
EVLHNSNDYVKEFYEHTVSNATDPSRNFNTLVAFPIKPSINDETTLLKADLANSVVQ
RMA

>YB039W, 1436 bp, CDS: 501-1436 (SEQ ID NO 41)

TTGAGATTTTCAAGATGATCACTTCTTCTAGTGTGCTATCAAAATPACTAAGGA
TAACTAATCTCTGTTTATACGATTTCTTCACTTATGCGTGAAGAGCGCATGTTTATG
TACATTTTCTAGACGTCGGAACGTAAGCAATGTGTCATTAACAAACAAAAAGTAAGA
GATATATGAATAGAGCTGTGCTGAAGAACTAGTATGATATGATGATGATGATGATG
AATTTTCGATATTTTATGAACGTTGCTATTTATTTGGAAGAAATGTTTATCAAGGATG
GAGAACCAATGAGCGGCGGATTAAGTATGATGATGATGATGATGATGATGATGATG
AGCCCGGAGGAGGATGCTTAAATGATATGATGATGATGATGATGATGATGATGATG
TATTTGAGACTGAACCGTTTGTGTTAATTTCAAGTGAAGAAATGTAAGACGAGCATAA

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CATTAATTAATTTAGTATGATGATGATGATGATGATGATGATGATGATGATGATG
TAAATGTCACCAAGCCAGTGGGTATCTTTTATGACATTAACCAAGAGAGAACTATG
CTACTTTGAAGAGATGAGAAATGCGTTGAAATATCATCAAAATATTTGAAATATCCG
AAACTATGAAGATGTTGTCATCTACAGATGATGATGATGATGATGATGATGATGATG
CAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ATGTTGAGGCTACTGAAGAGATGCTCTTGAAGATGATGATGATGATGATGATGATG
AGGGTGTGTGTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATG
ATCAACCAACGCGATATGATGATGATGATGATGATGATGATGATGATGATGATG
CCCATCTTACCAATTAATTTGATGATGATGATGATGATGATGATGATGATGATG
AAGATCTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG
AGATTTCCATTTTCTGAAATGACCGATGATGATGATGATGATGATGATGATGATG
CGATCTTGAAGCGCCACATGATGAACATTCCTATCTTGTGAACATGATGATGATG
CGAGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
CAATGCGTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATG
CCAGATAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG
CTGTCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG

>YB039W, 311 aa (SEQ ID NO 42)

MLSRVSNNAHTRSWMOHQAQVGLYKTNPVRTATYKEVEMELKSIKNIETKTMKIVA
STRLSKAERAKLSAKTMDABQLFYKNAETKNDVEATENGAPRELVAITSDDKLGSI
HSQLAIVRHLINDQNDIVLTDGKIKQMLTHTPNNIKLSINGIGDAPFPQBSALJA
DKLSVMAKGTTPKISIFPNDPVSSLSFSESEKPIFNAKTEQSFSEKFEIDTANVPR
DLFEYTLAQMILPMAQGYAAELISARRNADNASKMAGDMINRSILVNRHQAVLTNEL
VDIITGASSLSG

>YB062C, 848 bp, CDS: 501-848 (SEQ ID NO 45)

CCATTTTGGGACCACTCTCTACCCGAAATTAATGATGATGATGATGATGATGATG
TAGATTAATGCTTATTTGCTTAAAGTGTGTCAAATTTGTGTGGCGGCTTTTGTGCA
CCGAGAGCGCTTATGCTTATTAATACAGATTTTGCACCTTAACTGAATGAAGAT
AATGAAAGATTAATTCATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA
ATGATATGATATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA
TGCATCTCATTAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AGTAGAGGAACTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
TATTTCAAACTTTGTTGATCAACAGTGTGTGAGGTGATGATGATGATGATGATGATG
TTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TGGATTAAGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ACGATATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG
ACGTTAA

>YB062C, 115 aa (SEQ ID NO 46)

MLPESLQEWLQEMDKGASGPDFTFASLPIRINKKTKATNDSCICYNLYLEDEYPLV
ELPCHNHFTDLECSLWSLSTPCPLCRDVMGHRILNIEDTTAELEEDMGMYG

>YB101C, 1373 bp, CDS: 501-1373 (SEQ ID NO 49)

AATGATGAATGTTATCCCAAGGCTCATTAATGATGATGATGATGATGATGATGATG
AAGCGCGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG
AAAAATTCGTTAAACAAAGATCAAGAAAAATTAACCTCATTAATTAATTAATGATG
TAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
GTAAGCTTTTACCTACTGTGTGTGCAAGTTGGGCGGCTTAATTAATTAATTAATTA
TCGTTGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGAATGA
AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
AAAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

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GGGACAAAGAAGCTATGGCTAGGGCCGCCAACCTGATCTCTAAATGCTACAGCAGATTAT
ATCGGTGGTGGTCTTCCAGATCCAACTCTTAATGAAAGATTCATCTGCTGTTATATGAA
TCTGGGATGGTGTGACTTAGAACAAACAACTCGTGTGCATGACACCTTTGCAATCTGTTGATG
AGAACTTATAGATAATGCTTAATAATATCGAAATTTAAATCTCTGGGAGCCATGTTGTGGATG
TTCCTCTTCAGACGAGGATGAGCAACTACGTGCTGCTGCTTTATCTCATTTATTTGGAACGG
CTGTGCAAAACAACTTGGATTTGGCAAAATAATTTATGAATAAGCAGCAATGGTCTGCGCAA
GGCTTATCGAAATATGCTTAGCAGAACAAAGCCATCCGATCGAGATGAGAAACAAAGCTTTT
AGCAGCTATCTTATCTTAATAGAACACCAAGAATATCTTCAGAAAAGTTTTTTCAAATATA
ATGGGCTCGACTCATAGCACCTGTATTTAAGTGATTAACACGGCAACCAACCAATCTGAAAA
TCGAGGCCATTCGCTTATTTGACGCCATATTTTGTTCATCTGTTTAAAGTTCATGTAATAATATA
TCAGTGTGCTGAGAAAGGATGGAGATTTAAGAGTATCGATTTGGTGGCTGTCTGACAGAA
GTAACTTTGAACATCATATAGATAGAGTCTGCTCTTTCTCTCTCACCTCATATCTTCGCGGA
TAAAAATTTAATGAACAGGAATATGCAAAATTTGAACGAAAGTTTACAAACATCTTCAGCCCTC
TTAAGGACAGACTTAATGAAAGACGATTTATGCGGTAAAGGATCTATATGAA

>YBR101C, 290 aa (SEO ID NO 50)

MEKLLQWSTANSOGDKEMARAGQDPKLLQQLFGGGPDPPLMKESMAVIMPEVDLE
TKLVAFDNFEMLTENLDNANNIENLKLWEPLDVLVQTKDEELRAALSITGTAVQNNLD
SQNNFMKDTGKPLJELIASDGTKPLPDVTKTQFALSNLIRHKKDISEKPFKJAGLDCIA
PQVPMYNTAGPLKQRAELATVILSSVYKIDENIIVLRSKQVITESTIECLSDSEMLNITID
RVLSPLSHLISSGIKFNEQEBLHKNEKYEIPIKORLNEDDYLAKVYL

>YBR139W, 207 bp, CDS: 501-207 (SEQ ID NO 55)

GGAGGAGTC AAGGGCC TGGAAAG TACGGAT CCTCTG TAGAAATAT CACTGGCAAT TATATCTG
AGTTTAT TGTGGTG TGTCTAT ATATAT TTAGCTGTG TATATGGACGAAACG CAGGATAT
GAGTTTGTCTACTACTTACCAACACCTTAGCTGGATTTGATCTTTTCTGCAATCTCTTTAA
TTTTAACCTTTATTTAGTGGTTGGATCTAAGTTTCTGGAGACTTATCCAAATCTGTGACTATG
TTGGATAAATAGTTTATTGACTCGTTTAGTATAATCTTTTCTTAAAGTGTCTTAGAGTT
CTCTAGATGTTCTCTGTATCAATGTGAGCGATATGCGTAATTTCTCTAAATATGGCCGAG
GCGGCGCTAGCAATCTACGAACCTGAGATACCGTTTACGTAATTTCTCTAAATATGTCACGGGA
CAGGGTTATATAGAAACGAAATTTGTCTATCTCTGCAATTTTCTTTAAACACAGCTATACCA
AAAGATACCCGACATCAATAGAGTATCTTAACCTTAGTTTCTGTCTTCAAGATGATATACCACT
TTAGCATCAATACGCTCATCTCGCCGAGGCTTTTCTCTTTTGAAGATGATATACCACT
TTGGCCAAATTTGGATAAACAGCTTAAGCTTCCACAGAAATACACAGCAACCCCTTAATTTGG
ACCGTTTGAATCACAAGATGATCCGCTTTTACAACCTTTTATTTCTCTGTGGACACAGATTT
ACAGTTTGGAGCTTAGAACAGTATAGTCTTTCTTAACTTAGGAATATGACACCGCTTAACCAAT
GGTGGGTTACATGSCATATAAGGATTTCCAACACTTTTCTGGTTTACTGGTTTTTGTGAAGATA
GGAAACGATCTCTTAACGACCCTAATATATCTTGGTTTAAATGGTGGTCTGCTGTTTGTCTT
TCCAATATCCCTATTTCTTGGGAATATAACGGTTCAATGATCTTTTAGAACAGCCCAAGATCG
GAGTCGGCTTTCTCTATTTAGAACTAGGCCCTCCATCAATATGCTCTTACAAATTTAGAACAGCAAGATG
CGTACATTTTCTCGGAATTTGTTTTTGAAGTTTTCTCTATTTAGCCTCCACGATTTCC
ACAAGCAGGCAATCTTATGACGAGCAATATATATCTCTCTAAATGACATAGCATGCTGTAG
TCAAGAACCTCTGAAGAAGCTTACATTTACTTCACTTATGATTTGGTATGTTGATATCATCAG
ACCTTTCTCATCAAGCAGATATATATGAACCAATGGCATGGGGAAGAGGGGCTATCCACC
CTGTTCTCATCAGAAAGATCTGTAGAAATAGTATAAGCTGCAGCTCTGTGTCTGTAGGT
TGAACAAGTTATGTTTATGCTTAAATCAAGTTTATACCATAGCATGTGCCACTGCTTACT
GTACCTGTGCATTTTGGCAACCGTACATTAACACAGGACTCAACGCTTATGACATAGAG
GGCCCTGTGAAGATAATATAGTACTGTAGTATGTTTATACAGTCTCTCCGCTATCTGACC
AGTATATGAATTTTCTCGAAGTTTCAAGAAACGCTTAGGCTCCGACGTGCATATATATCTCTG
CTGTGATATATGACGTGTCTACCGGATTTTTGTTTTACGGGCAATGGAAGTAACCAATTTCTG
AACATATATATTTCTGTAATTTATTAATAACATAAAATCTCGGTATTAATATATCGGCTGATA
AGGATATATTTGTGTAATTTGGCTGGGAAAACAATGCTTGTGCTCAATGAGTTTGGAAATGGAATCA
ATTAACGCTAGTATACAGAAAGATTTAGAACCATAGGCTAGTAAGAAACACAGGTGGAAG
AGTTGGGACAGTCAAGAACTATGGCCCTTTACCTTTTGTGGAATATAGATGCGCGGTC
ATATGTGGCCCTATGATCAACCGGAGCAAGTTTGGAAATGTCTAACAGCTGGAATTTCCG

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GTAATCGTGCTTTTTCGGATCTTTCCACCTTGGAAAAATGCTAGTTAG

>YBR139W, 508 aa (SEQ ID NO 56)

MKYLNLVFVLQLLSIKYASFGRAFSLFEDDTTFANLDKQLPQNTQOTLKLDRLNHDH
 PLFTTFISGVDVDSLRURTVDYPSKLGIDTVQWGSYMDYKDSKHFYWPFPESRNDPAND
 PIIUWNLGKGCSSPTGLFELGSPISGADMRPHNPYWNNAHSIFLQPLGVGFSGY
 DEKVSUWLAGGADYFLLELPEAPSHLRNDFHTAGESYAGHYIPIQIAHEIUVNPNP
 PNL'YSMTNGITDPLIQADYYEPMACGGGYHVLSSCEKMSKAAGRCRRUNKLCA
 SKSSLPCIVATAYCDSALLEPYINTGLAVYDTRGCEDNSTGCHYGLRYDVQYMNPP
 VQHTLSGDVHNYSGCDNRDVTFTLPTGDSKFPQYVIAELLAHNIIPVLIYAGDKDYICW
 LGNHAWSNELHINKRYYQRRMLRPMWKSCTGEEELGQVKNYGPPTFLRIYDAGHVPYDQ
 PEASLEWNSNIGRAFSDJSTLEWAS

>YCL052C, 1751 bp, CDS: 501-1751 (SEQ ID NO 67)

TCCACATGTTGAGTATGCGTATGCGCATTTCCCTATCTTGTGAGRAGGAGTATGAAAATAAT
TCCGAGGGTTCAGATGCTCTTTTGTAGAAATAAATAAGATGTAAATAGTTGGAAATGTAAT
CTTTAGTAGACAAATGACGGTAACTTTAGTGGCCCTTTGCGGATTTTAAACAGTATGCTCTTT
AGTGCAAAACACAGAAAGAGCTCCCAATCTTTGTGAACAAATCGACCACGGAGGAACAATA
CAGCTAGAAGGGGATACTAAACACTTTGTCTGTCGACAGATTTGTGAGGACACACTAACAG
CAGAACTTTGCCCTTCTTAACTCTCTGTTTATGATTGCTTGAAGTATTACACATGTAATAAA
AGATGATATTATTTTTTTTTTCCCTTAAAAAAGTTCTTTCTTTGAAGATCCCCCTGTATAAAA
AAGATCAATAATGGAACCGTATCATATCAATCAATCGGGAGAGAAATAAACGCAAGAC
TGTGCGTTTCTAGCTGAGTATGTGACACAGACATAGAGTGACGTACTCTACAACTGCC
CTGAGATATCGGTATATCATATGCCCCAAAATGACATCTATTTGACTGTCTGTGCGAGGTT
TTAGTGTTGTTTATCAACAAGGTGGCTATTAGAGGAGGACTTGAAGCTTTAGCGTAATCTCT
TTACAGAGATCACTTGGAGGCCGAGCGGCACTTGGCTAGAAAGCTTTAGCGTTATAGAAA
ATGAATCTAGTGTGCTGCTCTTACGTTTCAAAATCTTCCGATGTCGAGGAAAGTATTA
TTACTAACCCAGTCTACAATCTATTACAGTGAAGAGTTTGACATAGACGAGTACTTGC
CTCCGAGTAGATTTGAATCTGTCTCATCGAATCCAGAGAATTTTACATATGATATATCAG
TGGAGCCCAACAAATCCAAATGTTGTGAATATCTGTCTGTTTGAACAGGGTGAAGAATTTA
CAATTTGACAGGTGAAGATGAGAACTCGAAGTAGTGTATCTTTGTGGAATGCAAGTG
ATGAAAGTATGTCGATATTGTTGGAAATCATGTTGATATAAACAGGGCCATATCGCATACATCACT
TGGAAAGAATGCAGAAAACATCTTTATTGTATATAACAGGGCCATATCGCATACATCACT
CGACACTACGACATCTCATATGTAATGAACCTTATCGTTGCACTCCMAAAATCATGA
TGTGATCTCACAGATTGAGAAACGCCCTCAATGCTATCTAAATGACACCTTGGCAATGCG
CGTTAGAATTATTTATCGATAAATTCCAATCTCTCCCTTACTTACTTACTTGGCAAGACG
ACTTTAGAATTACCAGAAATCTCTCTTCGAGATAAGGCATGGGGTTCGAAAGTATCTTTTG
AATTAAGGGGACACATGAATGAAGTGACATGCAATGCAATATATTGAGCCCTTCTTA
ATATAAAGGGGATAATTTAGAAGTTTCAATTTGATCCAGAAAGCTTAGGATATGATATCTC
CAGGTGACAAATAAAGTTTCCCGTAATCCATTTTATAAAAAGCTTAGGATATGATATCTC
TCTTTACAGACGATACATATTCGCGCAATTTGAATCGACAACTCTTCTAGTACCAATTC
CAAGGCCCTGACAAAGGATATTTCGAAGATCAAAAAATGGTAGCTTACTATGCTTACTCA
TCTCCAATCATATACATTTTCTCCAGGTATTTTGTTAACAAAGAGAAAGATCATGATA
AACGGGATAA

>YCL052C, 416 aa (SEQ ID NO 68)

MYTRHRVTVLYNAPEDIGNHMQNDTHLTVRGSGVVLOQRWLLERTGSLDKSFTTRITWR
PRADRLSIVTENLSAGFVYSNSDVPERFITNPVNSPHSEKFDIOEYLPPEVDLN
LSWNPEDFTYISVPTQIQIYEYRLTKQGEFTIARVDEKLEVGUFVDADESODVDI
GGICRNWRMDGKMERCKQTSLLYKQGHYAYNHSTTISLYLNEPTLGHFKMTIDTDFE
BRPKMILMHQILQPLELFDKQSSPLFLGEDDLEPEVSLRDKAWGSSGISELPELKACTM
NEVTLHTHYIPEPSNNKDKLEVSFDPEVTLTACTGDNKYSRNFPIYKGLGYSLEVLTDFTT
FHLNLSSTLLVPIPRDRTKQVSKINGNKLCLLSIIYIFSKYFVGNKKRKSVRKE

>YCR009C, 1298 bp, CDS: 501-1298 (SEQ ID NO 73)

GTACAAAAATGATTACGAAATATAGATGATGTAGCAAGGTACGGTTATAACAGTTAA

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CGAAACCACTGATCTCTCAGCCCTCTCAGCTAGCCAAACAGCAGCAGCAACCTCCACAGGATA
TTCTTCTAAACTCTATCTCTCTCTGCGCAAGAGTGTTCGAGATATGGTAG

>YDR073W, 169 aa (SEQ ID NO 92)

MSSEIAYSNVTNNTENENRNTGVDVNTNANANANANATANATANATANAELNLPVDE
QRQYKQLLLHNSILLARVIQNNNSIQNNLNQNNINNNNNIIIRIQQLISQFLKRVHAN
LQCSIQNGVPSAKPLILTPQLANQQPPQDILSKLYLLARVFEIW

>YDR178W, 1046 bp, CDS: 501-1046 (SEQ ID NO 105)

ACGATTAGCGGCTCAAGTCTCTAGACCCCAATGACAACAACAGCAGCCGCTATCATCGA
GGAATGTTGAAGTGAATAGATAAAAAAAGCCACCAAGTAAGTAAATAAAGAA
TAAATAAACTATAATAGTAAACAACCAAGCGAGGATGTTTCATTGTGCACTCGTGTCTT
GATGATACATATAGCTGAAGAATTAATACGGCACGTTAAATTTATTTAGAAATATA
AACACTTTATGTGCCATAAGCATGAGCCAAATCGCTGCTTTTTTTTTTTATTCGGGGCAC
CTTCGGAAGAACAACAGCGCAATTTAGTATATAAGGAGAAGCCCTCAGCGCATCAGGG
ACCGACTCGGATCGCTTTAAGGCAAGATAGAAGGATAAATATCTGCTTTGGAAGATAG
TCGTAATTAATTTCCATCTCTGTTGTTGTTGATCTTTCTGATCTTTCTGACTTTCTTC
CTACGCGCTTTATAAGCTATGATGTGCAAGATCCATGAAATTTATGACTGGAAGA
GAATTTTCCATACCTGCCACAGTAAGGCCCTTCCAGTCTACCGCTAAGAGAGCTTAACTA
TCCCAATTTTGGCCGTTATACCCAGAAACCAAGTGTGTGTAGGGCACTCCCAATGATG
CTTATGCTCCCCCTTGAGAAATAATAGAGGCTCATACCACTGATATGGAAGAAA
TCTTTGCTGTGCGCTGCTCAATGGCTACGACGCTATGCTGACACCGCTCGTTAT
CCACTGACGCTGATCTTTCTTCTGCTATGCTTTTGGGATATGTTTACATGGAATTTA
ACTCTGTATCACCGATATATTTCTGAAAGATTTATGTTGTTGGCCACAGTACGCCA
TGTATATTTGGGCTGTGCTGCGCTTCCCTTTTGGAAATCTATAAATCAGAAACCG
AGAATGATGTTGTTGTTGTAGTAAAGTCTATGCGGATCTTCTCCGAGAAGACACA
GTCAAAAGATTGAAGCCAAAGTAG

>YDR178W, 181 aa (SEQ ID NO 106)

MLPRSNKFMTRRIIFHTATVRAFQSTAKSLTIPLPVLPLQKPGVGRTPNDAYVPPPE
NKLEGSYHWYMEKIFALSVPLATAMLTTGPLSTADSFVSMLLGYCYMEFNSCIDY
ISERVYGVHWKYAMTMLGLGSVSLFGIYKLETENDGVGLVLSWDSERDNSQKIEAK
K

>YDR202C, 1556 bp, CDS: 501-1556 (SEQ ID NO 107)

GAATTTCAACCGGAATTTGCAACAGCAGCAATTTCTCGTACCATGAAGGGGAACATGG
CGGTGTACCGAGGTTCATTGGCGGAGTATTAGCCAGGCCCTTAATACGTAACCTCGGTA
CGCTCTTCAGCTCTTTTCGCAATAATCAAGTCTCTGTTGTTATGTAATCAACAGTTCCATG
GATCCGCCAACTCTGCTCTCTTACCAATAATTAATGAGCCTAAGGTTACATTGCCGCC
GAGGTAAATATTAGCCACAGCTTGGCATTTTCACATGGCAAGTAGCTGTTGATCTCAGT
AAGATAACTTCAACATACTCTTTTACTTGTCTCTTTTGTAGTAAATTTGCTCTCTCC
CTTCTTTTCCAAACCCCACTATTTTCTCTCAAAAGTTATATGAAGTATATATATCTG
AATGGAGCAATTCGGGTGTAGTGAATTAACAAATTTATAGTATCTGATCAAGACACAGT
GGAAGTGTCTGAAAGCAATAATAGTGTGTAATTTGTTTCCAAATAGATATTTGTGTCAG
AAGATAATACGACAATTTAAGGATCGCGTAAAGAAATGCTCTCGCTCATCGAAGAA
TCGTCAAAACCCCAATTTACCAACATTTATGACAACCTTTTCTTAATAGATAGCTAG
AGAGTGACCAAAATATCAAAATGCTGTATTAATGTTATTTCCAAAGCAATACAAAC
AAAAACGCTCTCCAGCGTAAAGGGTGTATCACAGACAGGCCAATACATTGTTGACT
TTCAATTTGTGTGAGATTCCCAATTTCAAGGGGTAAACAAGTTATGTTTCCGAAATGA
ATACGGGACTGAAITTTCTTCTTATTTCAATTCAGTAAAGTAAATGACCGCACTTGAATAA
TTTTGAAATFACTGAATCACTCAAGTAGCTACAGATGTCAGCGAATTCGTATCCAAAT
TTGGCGGTGGCCATCGAACTTTTGAACCATCTCTAATACTTTTACAAAATCCTCCTAGAG
ACCTGGTATTTCCCAAGAGTAAACATTTGGCTATGTAAGGAAATGTTCAGGATTTGTACT
CAGTCTCGGAATCCACAGATCAACATCTCTAGGACTGGAACCTTACGCTTTAGGATGAGC
TTTGCATAGAACTACGAAATCTAATTAAGGTGACTTAAACCTTGTGTGCGAGATTGATA
GTAAACCTGCGAGCTATTTTTCGACCAAAATAGAATCAAGTACAAAATCGAAGAAACA

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AAACTTTATCTAAGATCTCTCAGAAAACGGGTACAAAGTCCAGGATTCACACATTACTTA
ACCACATATTTCTTCTTTTCAAGTGAAGCTATAAAGCTTCCAGAGCTCAGAAATAT
TAAAGAGGGCGTTACTTTTCGATAATAGGGTAGTCAATGGAATGTGAAAAGTAAATATAT
CTAAGTGAATCAACTTTGATCATGATATAAGCGCCAAATTAAGAACAGTCTCAAAAGCTTCGA
TGGCGAACCATCAAGCAAAATTTGCTAGCTAGCAAAACAGTTAAGTACATATATAAGTAA

>YDR202C, 351 aa (SEQ ID NO 108)

MSVDLPNDRFGABDKYDNFKDAVKECSWLEIEIVKPOLPNIIDNPSKCLEMLESDQIFK
MFVSNQIWNHNSKNDSPVTKGVITRQGVIVDFVHFVRFQFQKQVQFMRNVTGLNFL
LQFSKIMTHLNLILSEIQLQVATVSEFVSKFVAMELLNHSLLILQNPPDLVFPED
NNFAMKEMFQDCVSCESTAHILGLEULICRNELCIELNLIKVTKPKWCEIDSKGRSP
CDQIRNVNERNKTKLSKILSENGVQVQDSTLLNHIISSFSQSEAITLPEAQELLRRGVTF
DNRVMECEKLVSTSDPTLSISAKLNSLKASHANQANLVASKQLSTYK

>YDR256C, 2048 bp, CDS: 501-2048 (SEQ ID NO 115)

GGGAAGAACTAAGAGATGTTATGCTCGGAGAGTTTTGAAGAAGCAAAATAGATATCCCTGC
AAGTTTGTGAAGAAACCATCGACAAGAAATTACAAGGTTATTCTCGATGAAAAGCTGTAA
CTAATATTTTAAAGAAAGTTGACAGAGAAAGAAAAGCTCTGTCAAAAGCTCTCTGGC
TGAAGAAGTACGCGGTGTTCTTAACCACTATTAAAGCCCAATTTAGTAAATGCAAAAAGT
TGGCGGGAATTAAGCCGCGCAAGTTGTGGGGTCCCTTAATCCGAAAAGAGCGGCTTTAA
CAAAATATAAATCCGAAAATCCCAAGTACAGATAATTCGAAAGAAACCAACAGTTTGTGATA
TCGCCATACATATAAAGATGTGAAGACATTTCTTCACTGTAAATGTAATAGTACTTACAA
TTGAATTTTCTAGCTTTATTTAAAGGTAAAGTAAATAATATAATAGTACTTACAAA
TAAATTTGGAACCCCTAGAAAGTTCGAATTTGGGACAAGAAAATAATGAAGTAAATTTACT
CTGATTAAGAGAGATAGATGTTGCACAACCTCCACTGTGTAATCCAATCAATGAACCAT
TTGTCAACCAAGTATTTGGGAAACATGGCCCTTTGCTTTTGGCAAGATTTAATCTTAAATTT
ATTCTTTGGCTCATTTTCAACAGGAAATATTTCTTCAAGGAATCCACATGCTCATGTTT
CTGTGCTCTCGGCTATTTTGAAGTAAACCGATGACATTAATGATGTTATTTCTGTCTA
TGTATTAGTAAATTTGGGAAAAGAACGAAATGCTCTCAACAAGATTTTTCGACTGTGGGTG
ATAAAGTGTGCGGACAGCTGTGTGATCCAAAGGGGTTTGGCCCAAAATTTCTACACTG
AAGAAGGTAAATTTAGATTGGGTCTACAATAATACACCGGTATTTCTTTATCAGAGACCTT
CCAAGTTCCTCCTTTATCCACACAGAGAAGAAACCCCAAAACCAACCTTAAGGGATG
CTGATCTTTTGGGATTTCTCACCACTCTCGAAATCAGGTGCGCAATTCATCAAGTAA
TGATCTTTTTCAGACCGCTGCTCCCTGCAACATACGTTAGTATGCTATGTTATTTCTG
GTCACTACCTATAAATGTGCAATAAAGACGAGATTTGGCATTAATGTCAAGTTTCTATCTA
AAACCGATCAAGGAATAAAGAAATTTGACCATAGAAGAGCTACCAAAATTTGCGGATCA
ATCCAGATTACTTCCAGCAGGATTTATTTAGCTATTTCAAGATGGAATACTATCTCTCT
GGACAGTTATATTTCAAAATGACCGGAACGCGATGCCAAAAAATTTACCTTTTCACTCT
TTTGAATTTGACTTAAAGTATGGCTCAGGGCAATTTCCCTTTTACGGCGTGTGGGTAAGATTG
TTTTGAAGGAAATCCACTGAACTTCTTCACAGAGTGGAAACAGAGCTGCTTCCGCCCA
GTACCCAGGTTCTTATCAAGAAAGCAAGCGCTCATCCAGTATTACAGGCCCGTTTGT
CATATGCGGATGCTCATAGATACAGCTAGGCTCTAACTTCTCAATCAAAATGCCCGTAAACG
GTCCATATGCTATATAATTTTCAATCCGCTATCAGAGATGGAACCGATGAATGTTAACTG
GCAATCTCGGCTCAGAACCTACATATTTGGCCCAACGATTAATCGTACAGTATATCTCAAC
AGGACACACCATTTCAACAACACCAAGAGTATGGAATGGGCCAGCTATCTCTTATCTATT
GGGCAACATCCCGAGTATAGATTCTCGTCAAGCAAGAAATCTCTACCGCGCTTTTGG
GTAAACAACCTCAGCAGCAAACTTGGCATATAAATCAATCGGCAATTCATGTAGAGCGG
CCTGTCTCAAAATACAGCAGCGCTTTATGATATGTTTGTCTGCTGTTGATGAAGGAGCTAT
CTGAGGCAATTTAAAAAAGTAGCTGAGGCAAAACATGCTTCTGAGCTTTCGAGTAACTCA
AATTTTGA

>YDR256C, 515 aa (SEQ ID NO 116)

MSKLGGEKNEVNYSDVRDVRVNTSGNPINEPFTVQRIGEHPFLLLQDYNLIDSLAHFN
RENIPOBNPHAHGSGAFYFVETDDITDICSAMFSKIGKRTKLTCLTRFSTVGGDKGSDAT
VRDPRGFATKFTYEEGNLDWVYVNTVPFPIRDPSPKPHFIHTQKRNPNQTNLRDADWFDF
LTTPENQVAIHQVNIILFSDRGTPANYRSMHGYSGHTYKWSNKNQDMWHYVQVHIKTQDGIK

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ATAATTGCAAAAACCGAATGCGCGCCGCCCTCACGCGGAGCGGAGAAAGAGGCGCGGT
CCCCGTTTTTCTGCTTTTGGCTCATCTCTTTGGCTCCGACGCGAGCAAGCGGATTCCTC
CCTCCGCTGCTTTTATTAATAACAAGTCTCATCTCTGCTCTCTTTGTTCCGCTC
GTTGCGGTACATTTTACGTGATTTATCCCAACCCCAAGAAAGAAATTTGCTACATCTGCA
TCTGCAGATTTATTTAGCTTACTTATCTCCATTTGTTAGCAGTATTCGAAAGTGAAGATAT
ATCAGATCAAGTATATAGTATGACAGAACTTACTTTTAAGAAATTCACGCGGACCTTA
CGGCTCTCAATTTACAGAACCCCGCCACCACCATCTACACCAAGAGTAGATTTCTTG
GGAAGGCTGCTTACAGCTTTTAGGAGAAGTCTGCTGAGCTTTGTTGCGCCAGAAAT
TATCCAGAAAGTTGCTCAATTTGTTAGATTTGAAGAAAGTCTTTTGGGGTTGGAAGACG
TGACAGCCAAAGAACGCTGACCTGCTAAGCAATTTCTATTTTGGGGTTGGAAGACG
ATGACGATCTTCCGACATCACTGATBAATTTAGGTGCTCTGATCTATGAATTTAGTGAAT
TAGACGAAGATTTATGCTGTTATGACCAATACAGATTTGACTTAAAGTCCATCAGAG
ATATCGAACCTTTCTTTCACCACTAGAGACCGTAAAGCAGAGTACCAGCAAAATCG
CCTACTTGAATACAAAGATCTCAATCACCTAAGATTTGAGTCTTGGAAACAGAAATGCG
TGGCTGCTGAGGCTGAATCTTTGCTGCTGAAGCTCAATTTATCTATATCAAGGCTCAA
AGTTGAGAGCTGCTTTTCACTTACCAATTTGACTCCATCATCGAATTCAGAGAAATTTG
CTTTAATCGCTGCTAGGTTAGGCTCTCTTTGGAATCTATTTGACACACTCTCTGCTACTC
CAGGTGAAACCGAGGCTGCTTACGATGGGTATGAAGCTCTTAAACAAATCATTTATGATG
CTGAAGCGCACTGAATGACACTAGACTCTGCCCCAAGTCAAGCTACTCTTTAAGTT
TCAAGGAGATTCAGAGACTTCGAACCTTGAAGAGCGCAAGAGGAGGAGGAGAGCG
GTCAAGGAGCTGGTCCGAGACGACAAAGAGTGGACAAATTCGAACACCTGAACAG
AAGAAGAGGCTGTTGTAAGACATGAACAAGTCCGACACCAAGCAAGTGAAGTCTCTTC
CCCCAACAAACACGCTTAA

>YGR086C, 339 aa (SEQ ID NO 176)

MHRTYSLRNSRAPTSQLOQNPFPSTTKGRFFGKGLAYFSRRAAGAFGLPGLSKLSQ
LVKLEKNVLRSMELTANERDAKQLSINGLENDVSDITDKLVLYEVELDDQFID
RYDYRLTLKLSIRDSVQSPDRDKDIIDKLAFLKYKQPSKPIEVLLEOELVRAEBS
LVAAELSNITSLKRAAFYQFDSIIHSEKIALIAGYKALLELDDSDSPVTPGETRPA
YDGEASQKIIIDAESALNEWTLDSQVKPLSPFKQDYEDPEPEGEDEEDGQGRWSE
DEQEDGQIEEPQEBEGVAZEHEQVGHQSESLEPQQTTA

>YGR197C, 2144 bp, CDS: 501-2144 (SEQ ID NO 185)

TCAGTATGCCACACATATATGCTTCACACCTAAAGCACATATTTTCGTTATTTTTCAC
CACAAATGATGCTCGAAGAGGATGGAABATCAGGAAAGAAATGTTGAGAAAAA
TAAACCGATTCCTGTTTCTCTATTTCCGTGTATATGCGTGTATTTCTGTTTTC
GAATCTTTATGAATGTCGAGGAGTGCTACATCCGAATAGACTAAAGAAAGCA
AAGCCGTGAGTTTGTGATGATAGATGCTCGAGCTTTGTCATCAACGGGCCACCTA
TTCCAGAAAGGGAATGGAACCGACTGCGGTAGTCAATAGCGTCTTCATATCTTAGCA
TTGTTGAGAGATACATAGTGTACTCATATCTGTTCTTTTATTTATATATCAAGCCAC
ATATCTCTGTTCTTTAACTCTTTTATACCGCGTGAATCGGGTACTGACATAGTGTAG
TAGCCGTACAGAGAAACAAATGACTAAATCGGTGTGATGAAGAGTACAGATACATTTG
AGGACCTGATTTTCAGCAGCAGCTGCAATTTACTTGGCGGAGGACGGGTTTCTGTA
GTAATCGCGATTCGTAGGTTGCTGGCCATCTTCTGACTAGCAAGTCAATTAGAG
ACTATCGGCTCTCTGATGAAGCCCTGCTCATATGTCATCTGTCGGGGAAGTGGGCTA
ATGAGGAAGAGAGGGCGGTAAAGCGGGCTCCCTTGGCAAGAAATCAAAAGCGGCTTT
TTTTCTCAAGACTGCGAAATCATAGGAABAAAGATCTCTCGAAGTTGTTTGAACAAC
TCTCTATGCTTGTCTTTTAACTCTTTTATACGATATCTGTTATTTGAGGCTGCTGTTACGGA
CAGATCTGTTCTTTTCAAGGTGAATAATTTGTTATTTAGCGGTCTGTCGCCGGAGAT
CTTCAGTTCATCTATTTCCCGGATACATCCCTCATTTGTTAGCTGTCGCCGGCTCTAATA
GGCATATACACCGCAACATCTTTCATAGGAATTTGTTACACGACCTCCACCGGAA
TTGACAGAAAGATAGTCGATTAATTTAGCATGAGATATCTGCTGCGCTTTAAACGTTA
TACCTAATGCTACAGACACTTTGTTAATTTCTTTGATTAGCCAGACGCAAACTCGGAGT
TCAATTCATCAATTTTGTGAATCGGTGTTGAAGTGTGCGTGCACCATCGAGTTTA
AATCGACCAATTTCTACCACTCATGCAACATTTGGAGGTCGCCCTTCAGAAATATTACGTCA
AGGAATATCTTTCCCTCATTTGATGAGCAACATCATCTTCTAATGACAGAGATCTTAAATATA

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ACATGAGAGAACTGPGCGGATTCGAGGACAGTTGTTGTTTTCACCTACACGATTTATCGTCCCT
TTGCTGATCGTATTTCTAATATGCCCCCTCTGACGTCGCTGATTTATTTGTTATTTTGTAA
CCGTTTTACAACATGCTCATTTATATGTAAGTTGACGGAAGAAATGGCCAGAGTTCTGAAGC
CAAGACATATTTTATATACAGGCTTCTAATTTCTCTGGCACTTATTTTCTCTCTTTCCA
TTGGAATTCGTACCGTATCTGCAATTTTATAGATCGATTTTACCCCGCTTTTGGCAGAG
GAGGATTCGTATATTTGGAATGCTCTACGTGTTGTTGTTAATGATGGCTGTTGTTGGTGCCA
ATGAACAGTTTCTCAGCTTTAGTTATATAGCTTTACTGCCCCCTCTACCTGAGTATTTGGTTGA
TGACGTGATCATATTAATATTTCTGCTTCTATCTACCCAAATGGTTTGAACAACGAAT
TTTACAGATCGGCTACATAATCCATAATCCATAATGCGCGGTGATATCTATAAAGTGAATTT
TTTTGAATTTAAACCAAGAAAAATGGGAAGAAATTAACGTTATTTCTGTCGATCGGTTG
CCCTCAATACATCTCTGATGCCATTTTGTATGAAGTTTGCAGGTAAAAAATGCAAAAAA
ATGCTATGCAAGCAGCAGAGCGGCTGTCGACGAGCTACCCAGCGTGTAGTCCGCCCGG
CAGAGGCCCAATACTGATAAAAAATAACAACCCCGCGGAAATTTAA

>YGR197C, 547 aa (SEQ ID NO 186)

MTKSVGBEESQVIEDPSPFAAAAFVGGRDGVSYNQRFAGSGSHSLAKSLEDYRPDE
KPSLSVSGEGANEEKGGNDGGLARIQTLGFLSPRLNRHKKILSKFVLNFFIACVC
VSLISIVMGACGTDRYFVKVNIIVLQDAPSNVSQSI SAIIIPSLASVPVTHIYNAT
SFHRKFTGNTSTEDRKIVDLYDERYMLANVKPNATDTLYNSLSIQDANSEFNSSIFP
ESVPEGRDPSVSKSTILPLMQOLEVRQYVYKEVLP SLSMNSITSNDRDLNINMENWAI
AGQLLFYNDYRFPADRLMAPLQWGLIYCTILLTQLSLYGLHGEWAVLKPRIILY
RLIISWATYFLLSIGFTCSAISIFRIDFPAGRGGFVYVMSTWLVVMVAGGANENVLSL
VIAYCPPLYSIWLMTIILNISASFPYPMVLNNEFYGYIMPIHNAVVDIYKVFILNFKR
KGRNYGILVNWVALNTSLMPFCMKFAGKKMQKNAMQAAEAAVAAATQRASRPAAENTDK
NNNPPGN

>YGR250C, 2846 bp, CDS: 501-2846 (SEQ ID NO 191)

TCCTGTGTACGTACGATGTTTCTCCGCTGATCCGATTTACTAGCCGAAGAGGTAAAAATTG
GCCCTTGATTCAAATTTATGCTCCCTTCCCGGAATAGTTACCAAGGCAAAAAATTTCCAG
TCGGAGTTCCTTATTTGGCGGAATTTAGTAGTCTCTTTCGTGCTAATAGCCCTGCCCCG
TTAGTCGTTATTTTCCAGTTAACTTTTCTTGCCACTGCGCTATATAAAATAACATACAT
ATATATCTCAAGCACATAAAGAACTTCCCTTAAATATTTAATTAAGTAATTAATAGTTG
AAAAAGCTTGTTCGGAAGTATAGTAGTGTCTTAAATTTTAGTTCTGTTTCAACGGTCTC
AAAAAGTGTGAACAAGTAAGGATAGCACACACATCCCAATTTACAGGCACCTGATTA
AAATCCAAAATTAACCCATAAGTTTTATTTTACTAAAAACATTTATACGTGAAGACAAA
CCGATCAGAAAGTTTCGAGGATGAATATTCAGAGAACCATTCAGATGAAGTATATCTA
GTGCCCCGAGGATACAGATATCTGCAGCCAGCAGACATCAGCGCGCGCAGAGCTGGAG
ACCAATCAATAAAATTCAGAGGAAACTTCCACTGGTCTTCAACTGGAACAATTTGGCCA
ACACAAATTTTAAACCATAGAATAAATGGCAGTTACAGAAGAAAGAGATGATCACT
GCAACTCTAGAATAACCGATCAATAATGAGACACAATCAGCACATACAAAGGTATCTCCG
TTAACAACTCTGATACAGAAACATA TGAATTTTCTCCGATACAAAGGTTTACAGGTTT
TCGAACAAATAAAGACATCTATCTTTACGACATGGAAGTCAAGATATGAGAAATCTT
ACAAATACAGAGAGAGAGATGATGGAAGATAGTACCGTTTTCGAAGCACAAATTCAC
AGTACCCCAAGTCTTAGAAAATGCAATGTCATGATATCTCGGAATTTACTCAAGCGAAC
CTAGGTTAGCATATTTATTAATTTGCTGAGTGAACCAAGCATGCACTAACCTAATCTATC
CTGGAATAATTTTTCGGGGGATAGCAAGAGCTTCTTATTTGGTGAACTAAGTTTCT
TATTTTCAAAATTTGACCAATTTTCAATGAATAATGATATATGATATAAAGCAAGCGG
AACCTAAGCATACGGGTTCTCTCTCTACCTCCCTGGGTCTTCAAGTTCACTTTGCATCA
GAAAGATATGGAAGAGCGGTAAATGGCTCCACACTATTTTATCAACTATCACCTGAGC
GAAAGAGAGAGAAAGATTCATTTGGGACCATTCGCAAGAAACAAACATGATGATTAAT
TCAGGTGCTCTTTTATAGGCACTTGGCTTACAACTCTGAAAGAAATAGAGACTTTGA
TTACACTAAGAAAGTCTATAGAGTAAATCAAGAGAGTTTCAAAAAAGTTTTCGGACT
TTGATTCATTTTCTATTTACTTCTCCGAAGAGAGTAATACAGAAAGCAGTAGTTCTGAA
GTTTCAATGAGGAGGCTCAGTAGAATCAACAAATCTTCCCAATATATCTAATGAGAAATG
CCCAAGATGAAGATATGTTGAAGGTTATGTTTCAAGGTTTATGTTCAAGCTTATCAACCATGAAACAG
CACTAGCAGCCATCGAGACCTTTCATGAGGTTTCATGTTGGCATGGAACAGGCTCTGTTGTTA

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TTTAA

>YJL166W, 94 aa (SEQ ID NO 232)
MGPPSKTYNGWGHMGPGKQKGTISVAUSPYAQKPLQGFIFHNAVNSFRFRFKSQFLYVL
IPAGIYWMKNGNEYNEFLYSKAGRELEWV

>YKL117W, 1151 bp, CDS: 501-1151 (SEQ ID NO 247)
TTATAGAACTCTTTTATGTTTAAAGAGCTGTGTATAGTAATCTAAGTGAATAACACT
AACAGTAATAGCGGTGTGGCTAGTGGTGGCGCTCCCTAGCATGGGAGAGTCT
CGGTTCGATTCCGAGCTGCTCCAACTTTTATTAATTAATTAATTTTTCCTGCG
TTACTGCTTTTAAATACTCTTTATGAATACAGATATAATTTTGTATATACAA
GAGGTGACTGTATATCAATCTTAATTTGTGGTTATGTGTACATATACCTACAA
AGTTACCAACAACTGTTCGATCTTAATGTGTACCCGCTTCGAGTGTTTTGAAGGG
CGGAGGAGCGGCAAGAAATAGCATGGAAAGAAAGCAATAAAGAGCAATGGGTGGCAA
TGTATTAACTGTTCGAGAACTAGTGAGCTCAATTCATTACAAACAAGTTCCCAAG
ATCATCGATTCAATAGTCAATGTCGATGAAGTTATTAACCCCTCAAGTTGCATGGGCTC
AAAGTCTAGTACTACTGATCCAGAAAGAAATTTATCTTAACTATGTTGTCATTTGCG
ACTGTATGCCCTGAGTTAAACATTAAGCCATCATATCGAATTTAAAGGCTCAATCAA
AGCCTCATGTTGGGATGAATATCTCATCTAATTAATTAACATTTGATCTATACAGG
AAATTAACCTGAAACAAATGATGAAGTTGCTAATGGCCAGCACTACTTTTGAAT
TGTATAAAGGATTTAGAACTCTAATCTGACCACTGTTCGACAAAGGAAAGGTGAAGT
ACCTTACATCAAACTGATTTTCGATTAATGGGTGTATGAAGTCAACAAAGCAGAAATTG
AAGCTGAAGGTAAATAGTCCGCTCAGGAATGGATTTTCAGCCAAATGATGGGAGGTGCTG
GAGGTCTGGAGGTCTGGAGGCAATGACCTTACGCCAAATAATGATGGAGGTGTGGTGGG
CTGTGTTCCAGATATGGCTAATGACGAAATTAATGGCTCAAGCGGTGCTAATTTGG
ACATGGGAGATTTCAAGAAACGATGAAGATGAAGAGAGGAAATAGAGCCGGGAAG
TGAAGCTTAA

>YKL117W, 216 aa (SEQ ID NO 248)
MSDKVINQVAWAQRSTTDPERNYLVITVSIADCDAPELTIKPSYIELKQSKPHVGD
NVHHVQLHIDLYKEIPEKTMHKGQHVFLKYLKDLSEYWPRLTKVKYPIKTD
FDKWDEDEQDEVEABGNDAQGMDFSQMGGAGGAGGAGGDMFQNMGGAGGAGSPDMA
QLQLLAQSGGNLMDGDFKENDDEDEEIEPEVKA

>YKR075C, 1424 bp, CDS: 501-1424 (SEQ ID NO 257)
TTCAACAGAAATCCGTAGCGGAAACCGAAGCGGGGACAGTGAAGCGGTAGAGGG
GCGAGACAGGGGAACTTGAATGGGTATTTGCTTTTGTGCTGCAATTTTCCGCTGGTAC
CTCTATCTTTAGCGCACCGGAAATTAATCTATTTCTCATCTTTTCTTTTCTTTTCTCG
ACTCGATATCTTTTACAAAGAAACCCCGGGGAAATGTTAGATTTGAGCTTTTCTCCG
CAGGAAAGAAACCTGGGACATTAATCTTTGTTTTTCTTTCTTTCTTTTCTTTCTTTCC
TTGGATGACTGCGAGAAAGTACAGTTACCGGCTTTAGCAAAACAAACATATATATAT
ATATATGAAGCGTATGTTCAACGGTTTTATAGGTTTTTACTTTTGTGATTCAGTTTC
AACTTGGCCCTTCTTATCGCAATTCAGATACATACACAAAGTTTCATACACACACA
AATAGATACATATACAGAAATCATGATTGTGACGATACATAATTTCTGACCAAGATA
TAATGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AACTAAATCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACCTCGTTAGGCTACATCTTCCCTGAGGGGTGCTCATTAATCTATTAATCTATTAATCT
AGAACTTCAATCCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT
TGTACCGTCCAGATTTGATACATAGATAGTATGAAGAAAGCAATATCGCCGGTCCAGA
ACCAATATGACAGAAACAAAGAAATCTTAAATCTGCTTTAAGAAAGAAATACAGGAAT
GCTGGGTAAACCGAGGAGGTGATGATTAACGCTTCTATAGAGCAATGCAACAGCTT
TGGTAAATTTAGAGACATTTCTATGCCATCTGTTGATTTCTGATCAGCACTTCCATCTT
TGCACCAAGCTTCTACATGCACTAAATTTCTCCATAGTGAAGTTCTGAAGACCTTTA
TGAACGAAAGAGGAAATTTCCCGAGAGTTGAAGTTTAAACCAAGCGGTGATGAAGA
GGGAGATCGACTCAAGGGGACTATCCCGGAATCCCTCATCAACATATAACGATATCCAAAC

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ATTCCGGCCACCATCCGCGTACCATCGTCCCATCATCACCATCACCATCAAAATAGTT
CTCATTTGATGAACAATAAAGAGACTCATATATGATGCTCAGCAACTATACATTTGGCA
CTATGGAAGAAGACATTTTTTATAGGAACCCAGGTGTGTTTTTAA

>YKR075C, 307 aa (SEQ ID NO 258)
MTSLDDTTIISYQINIMLLDNMTNKNKPAIDYFHHFNDASLEISAWTLLKMRKHLRL
PSCSSDVLDDYNNYLVLRLHCLWRWSINHYGQNSKSNPLSINWNKETDVTVLVYGPDLT
NIDSNEETSPQNOIDQKQTNLKSALKNTECWTEVEVDEINASIESNDNALVKLEDI
SCPSSVDSHTSIPDQHSCTKTKSSIDEDSEDLMEKEQFPRLKFNQAVMKREIDSKG
TIRSSLINLINDIQHSRRHRRHRRHHHQNSSHSDETIKEAHYEPFNYTGTWNEEDIF
YRNQVVF

>YLR216C, 1616 bp, CDS: 501-1616 (SEQ ID NO 279)
GAAGAATACAAAGAGGTCCAAGAGAGCAAGACCCGATGTGTGGGACAGAGAAATATCC
AAGACCGGATGCTAGTAGAGAACTCTGCAATACAGCTGTGCCATGCCGAAACAGGTGAC
TGGAGCGATGCTTCAACGAGATGGCTTATTTAGGAAGTGTGGGAAAGAAATGTTAAT
AGAGACCGGTAAGCACAGTGGAGTGGGACGACCACTAAGGATTCGGAAAGAAAGTAA
AAATGAATACTAAATGTGTGATATACTTGTATATAATAGACAGCTGCGAGTATCG
AAACATATTTTCCCTTTATAGAACATAACTGTACGCTTTTGAACGGCATTTCTATGA
GCTTCTAGAAATTTTTCGCCCTAGCTGGAGAAAGTTTCAGACAGAAATTAATTAATA
AGTCGAATATCAGAGGTGCTGATGCTCACATACATAGAAACTTGTGAAGACAAATAT
CAGCGAATACAGGAGTAAATAGCTAGACCTTAAACCTTTTTTGTATATTTCTATTTGGAG
GTAAACCCAAAGCGGTATGATTTTTTGTAGTTGATCAATGATAGTATTTCTATTTGGAG
AAATTTTGTGAAGTTGTGTGAAGAAATCTGTGTATGGCAAGCACTAAACCTGATGTAC
CATTTGCTGACAGGGTCCATTTTCCACAGAGTGTATCAAGACCTTCATGTGTCAATTTG
GTGATTTTACCAATTTTAAATGTGTGTGCTGGGCTGAGACATATACATGCAAAATTCGAGG
ATGAAATTTCTACTGTTAAACATGATAAACCTTTCTTCTATTCATGCCCAACGCGCGTC
CAAATACCAATGGATCTCAAGCTTTCTATAACCTGTGTCTTCTACACCTATTTGGAGGGA
AGCAGTTGTGTTGGTGAAGTGAATCAAGGTAAAGAAATTTGCTGTGATTCGAAAC
AACAAATGACCAACAAACAAACAAACAAACCTTGGTGTGTAAGATTTGATGCTGCTGGG
TGTACTCTGAGTATTAAGTCCAGGAGATGCGAAGCTTACCAAGCTTACCAAGATGATGAGG
CGGATAATTAAGACATGTTTTTAAACAGACGAAAGTGTGACTTGAAGATTTTCGACA
CTGTTCTGGCTGCTTTAGAAATATGTCAATGTGATAATTTCTTGAAGATTTTCGAAAGATTTCC
CAGAAATTTGGAGAAAGAAATTTGAATAATGTGATAATTTCTTGAAGATTTTCGAAAGATTTCC
CAGAAATTTGGAGAAAGAAATTTGAATAATGTGATAATTTCTTGAAGATTTTCGAAAGATTTCC
TGAATATTTGCCATCTGCTCTTAAATTAAGATTTACAGCAAGTATTAGTAGCTCTCAT
CGAGGTGTTATATGCGGAGCGGTGACAAAGCCAAAGCGCCAAAGCTTTGTACCTGTC
GTGCCCTGGCTATTTACCATGTTAATGACACAGATATGGCTCTCAATGACCTAGAAATGG
CCACTATTTCCAGCCAAATGACGTGCTTGTGAAGCTATTTCAATATTAATTAATTA
AAAGAAAGCAACAAACGAAAGGCTTAAAGGCTCTCTTCTCGAAGATGTTCTCTCTGA

>YLR216C, 371 aa (SEQ ID NO 280)
MTRPKTFDISIGKPGQRIIVPELVNDIVPKTAENFKLCEGNAGMAKTKPDVPLSYKGS
IFHRVINDKFCQDFGFTNFGTGESIVDEKPEDENFTVKHDKRFFLLSMANAGPNTGSGQ
AFITVPTPHLDGKHVVEVQKRIIVRLIENQDCQENNKPLRDVKIDDCGVLDPDDYQ
VPENAEATPHLDGKHVVEVQKRIIVRLIENQDCQENNKPLRDVKIDDCGVLDPDDYQ
KYVKCKFLKEYPEDIEKEQIEKINQKVSIPLNIAICALKLKDYKQVLVASSEVLVAE
AADEKAKAKALYRRGLAYVYVNDTDMALNDLEWATTFQPNDAAILKAIHNTKLKRRKQNE
KAKKSLSKMFS

>YLR346C, 806 bp, CDS: 501-806 (SEQ ID NO 289)
CTTATCTCAGGTACCCATAATTTCAACCATCTTACCTTCCATTAATAAACACATAGT
TTCGTTACTAGCAGAGCGGTATCTGTAAATTTCTGCTTGGCAACACATCTTAGCTGAAG
TGAAGAGGACAGCGACCTGCTGAAATGCTCAACGTTTCTGTAATAATCCGCTATTTCCGC
GGAATCAATAGGCGTCTAGCAGCGCCCATCAATTTTCAGCGGTGCCGCTATTAATAATTA
ATTACCAAGATTTCTATTTCCGCGCTGATCTCTATCAATATTAAGTAAATCAATCTTTTC

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GAATTGGTTTGGATGCGCTGCTTCTGGTATACATCTCTGGTATGTTGATTCATAAATTCGCTT
CTATGACAAATGGTACCAATATTTCTATGTTAGAAATTTCTCTGGTATGCGTCTCGGTG
GTATTCGTGCTCTATCTCCAACTTGTATTCGGAACAGCACAAACACATTAGAGGTA
CCTGTGTTCTTCTATCTAGTTAATGACACCTCTAGTATTTTCTTAGGTTACTGTACCA
ACTATGGTACTAAGACTACTCCAAATCAGTTCAATGAGAGTGCCTTTGGGTTTGAAT
TTGCTTCTGGTATTTCTATGATGCTGCTGATCTTAATGTTTGGCAAACTCTCCAGATCT
TAGTCGAAAAGGAGATACGAGACGCTAAAGCTTCTTTTGGCAAACTCTCAACAAAGTCA
CCAATTGAAGATCCAAGTATGTTGCTGGAATGGAATACAAATTAATGACCAAGCTG
AAAGATTAGCGGTAAAGCTTCTTCTGGGTGAGTTATTTCTCCAAAGAGCTTGAACACTG
CTGCTGATTAAGGTTATGATTTGATTTCTTACAACTCTTACAACTTAACTGGTAACTTACT
TCTTCTATTATGTTACTACTATTTTCAAGCGCTGCTGATGAAAGATCTTTTCCAAACTT
CCAATCTTTAGGTATAGTCACTTTCGATCCACTTTCTGCGCTTATACACTGTTGATTA
AATTTGGTCTGTAAGTCTATTTGGGTGTTCTGCTTCCATGCGCAATTTGTTTGTGTA
TCTTCTCTACTGCTGCTGCTACAACTTATATCCAAATGTTAAAGATCAATCCACTTCCA
AGCTCCGGTAAAGTCATGATGTTCTTACCTGTTTATTCATTTTCTTCTTCCGCTATTA
GTTGGCCCCAAATTCCTACGTTATGTTGCGCAATCTATCTCTTGGCTGCTCAAAATC
GTGCTATGGCTATTTGCTTGGTGCCAACTGGATTTGGGGTTTCTTGAATGGTCTTCTCA
CTCCCTTCAATTACAGTCAATTCGATTTTTCATACGGGTATGCTTTCATGGGCTGTTGG
TATTTTCACTTCTACGTGTTTCTTCTGCTGTAACCAAGGGCTTAACTATAGAGG
AAGTTAATGAAATGATTTGAAGTGTCAAACTGCTCAAACTGCTGATCTGATCTCA
AAGAAAAAGAGTTTCCGAGGAATAA

>YMR011w, 541 aa (SEQ ID NO 304)

MSEFATSRVESGSGQTSIHSTPIVQKLEDESPIQTSKYTNABLPAKPIAAWTVVICLC
LMIAGFVGFGMDTGISGVNQDTFKRRFGQMSDGYLYLSDVRLTGILVIFNIGCAFQ
LTLGLRGLDMYRRIRGLMVLVIVIGVIQIATSSDKWQYQPIGRILISGMVGGLVILSP
TLISETAPKHIRTCTVSFYQLMIFLIGFYCTNYGTDYNSVWRVPLGLNFAFIEM
IAGMLVPEPSRPLVEKRGVEDAKRSLSKNVTIEDPSIVAEMDTIMANVETERLAGNA
SWGELFSKGA ILPRVIMGINIOSLQLTGNYPFYFGTTIFNAVGMKDSFQTSIVLGI
NFASTFVALYTVDFGRKRLCTGASMAICFVIFSTVGVTSIYPNGKDPQSSKAAGNV
IVFTCLFIPFPALSWAPIAVIVIAESPLRVKNRMAIAVGANWIMGLIFGTFPTPITSA
IGFSYGVYFMGCLVSPFFYVFFVFCETKGLTLEEVENMYVEGVKPMKSSGWSIKERKRVSE
E

>YMR099C, 1394 bp, CDS: 501-1394 (SEQ ID NO 307)

AACAGTTCACCTCGATCTACATATTTCAATGCGAGAAATGATTAATCTCTGCCATTTGAC
AAACAACCTTTTACTGCCAGCGCTTTCATACCATGATGTTTATATGCCCTAATTTATA
ATAAAGCATGACATAAATGCCAACCCCATATTTATATAGTTTAACTTGAAACCGAGATT
ATCTATTGACACGAGAAAGTGCCTTCTTCTTAAACATAAGTTAGTCCCGCCGACCATTTCA
TCTAAACCGCATCAATCATTTGACAGAGAAAGATGTTGTTAGATGTCCTCGTTCGCTAG
ACCGAGTCAATGATAACAAGTCTTTTCTCAAGCTGCTTTTCCATATAAAGAGTATCGCAA
ATGGGCTCACCAATGCGCTTTTATTTTTCACGCGCGAAAGAAACTTAGTAGCTCCCTAG
AAATGAATAAGAGGTGATTCGAGGTTCATATAAGCTTTTGGTAAACTTTGAACCAAG
AAAGATTAAACACACAGCAATCCCTATCAAGAAACTGATAAGAAAGTGTGTTTTCACCTC
ATCCAGCTGATGAGACACAGGTTCTATTTCTTAAAGTACGCTGCTACAGTTATTTCTT
GGAAATTTGAATCTGAAAGACAGTGTGTTGTTCTACTGCTTAAATTTGGATGTAGCA
AACCCTGAGAGGTGATACCTTTGGTCTTTCTGTTATTCGGGAAATAATAGCACCGATG
AACATTTAGTGAATTAATACCTCAACATGCTTTCGAAGAAATTTCTACTTTGGGAGTTTGG
GTCAACTAAGAAACCAACCGACCGTACAAATTTGGCTTGAACAGCAAAATTTGCTAAC
CAGAAATTTGACCAAAATTTGGCCAAATGATTTATCTTTGATTTTGTACTGTTGAATTAGGCT
CCGATTTTGTGAAAACCTGCCATAGAGATGAGAAACACATCTAGTTTCAAGGAAATTAAGT
TCAACTGCTGTTTCCATACATCTCTCGTATCGAAGATATTTGAAGAAACAAATGCTCTTA
ATTTAGCTGGCATGAACCTTTATGACCACTGTTGAAGAAATCTACGCTGCGCAAGCAC
CAGTCTTTTACCTTCAATGAAGAACCGATCTAAATTTATCAAGATCTGACGCGCGAAGCGG
CCATTTCAAATAGTTGACAGGGGCTTCAAAATTTCACTCTTAAAGATACAACTTTGCCCG
ACACTGTTGTTTGGAAATCCATGATGAGAGAGTCTCAAGGGATGCGCCGATTTTCGAACCAA

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AAACTGGTTTACCAACAAATGATGATTTGAACCTGGTCACTGTTTCATGATTTTATTTCTCT
TGGCTCTCGTGAATAAATGGAATGCTTTATCAATTTACTTTTGCAAGAGAAATTTGAAATATTC
AAGCTATTTCATAA

>YMR099C, 297 aa (SEQ ID NO 308)

MFIKETDKVELTHPDETTSVHLKYGATVYSWLKSEEQJMLSTAALDKSGSKPVRRGI
PLVPFVFGKNSDDEHLSKLPQHGLARNSTWFLGQTKENPPTVQFGLKPEIANPELTKLW
PNDYLLILVELGSDYLKTAIEVENTSSSKELKFNMLFHTYFRIEDIBGTWVSNLAGMKL
YDQLKESVYDHPVVFVFNQETDVIYQNVSAERAIOIVDKGVQIHLTKRYNLPTVWVNP
WTEKSGMADPEBKTVQQMICIIEPHVHDFISLAPGKKNMAYQLLCKBELKYQAIQ

>YMR110C, 2099 bp, CDS: 501-2099 (SEQ ID NO 311)

AAGACGAGAAAGCTAGATATATCATATACAGCAGCACATAGTATACCAAAATTCACGTACAG
GCACACGACAGATGATCAACACTTTAGAGGAAATGGAACAACGAATTTCCAGCGAAAAA
ATTTCCGAGTAGTTCATGATGAAAGATTTTACATGTCATTTTATATATAATATATACCGT
CCTATATGGAATTTACGCAACAGGGTATATAAGAACATTAACCCGGTGTACTGATATAT
CAACTATCGACCTCCAAAGCTTTTATCTATCAGTCAATTTTACATCAAGATCCCACTTTTA
GATAGTTCGAAAAATTCAAATCTAATATATAGTGAATTTAATTAGATGGTGGATTTGCTTACCC
TTTTTTTGTGCTTTAGGAGGAGATTTCTTGGATTTTAGGGATAAACGGATATTTCTAAACCAATG
TATAAAAACAAACTCTAGGCAATTTGATTTCTTAAAGGAATATTTCTAAACCAATGAGC
CATAGTAATTTATACCAACATGTCAAACGACGCTCAAAATATTTGAATTTATATATATATAT
TGCTTAAATATAGTGAATTTGAAATCTCAAGAAATTTCTTCTTTGAGAAACAAATTTGA
AATGTGCCACGAAATACCCAAAGGAAAGAAAGTCTAGTAATTTAGGCAAGTTGCAAGTGA
AAAACTCTATTATTCGGTCAAGAGTATGAGGAAGAACTGATGCTGATGCTATGTACAAAG
ACTTCTATCGGAACAAATTTGAATTCGGTCTGTAATGAAACGACCAAACTTATGAACGATA
TACTTCACTAATGAGATTTTACAAATTTGATCAAACTCCGCGGAGAGTATCTGATCTTCT
CTCTCTCAATTTGTTGGTAAAAACAATCTGTCAGAAAAATATCAAGGGCGAGTCTTTGA
TTATTTGCTCTTCAATTTTCCCTACTTTTACATTTTGGCATTTGCCCATTTGCCAGCAGCTTTG
TCCAGGTAAACACCAATGTTCTGAGCCAGTGAACCTAACAACACACACACTGCTGCTAGTTA
TGGAATAATTTGTTAAACAGCTGTTTCTGCTGAGATTTGATTTCAAGTAGTTTCAAGGAG
CTATAGATTTGATTAACAAGACTACTAGATTTGGAATAATTTGACCTAAATTTCTACACAG
GTTCTCCCGTGTGCGATCAATAGTTGCTGAGAAAGCAGCAAAAGTCTTAACACCTTTGTG
TACTTGAACCTTGTGTTAAATTCACCTTCTTATTTATACAGAAAAATTTTCAAGCAAGTAACA
TAAAAATTTGCTTTGAAAAGGATTTTCTTGGTCTTTTGGGAAATTTCTGGCCAGATTTTGTG
TTTTCCAGCATTTATTTTGTGTATACATAAATCTATCTATCCAAAGTCAATTAAGAGTGTG
AATCAGTACTATAATGAAATTTTATCCAAGCTTTGATGAAACAACAGATTTTCACTCGTATGA
TTCTAGAGCTCTTTACAAAGGCGTTGCAAGTATAAATCAACTCAACTAACCGCTCCAAAG
TTGTGCTTCAAAATTTCTATCAATTCAGATCTGAGGATCTATGCTCTTGTATGCCCAA
CCATAGTTTATAACAATTTGTTGGGATGATCTTTGATGAAACAGGAAACCTTTGCTCTCTG
TATTTGCCCATTTGATGATGAGGATCTTTGATGAGACCATTTAACAGATTAATAGAGAAC
ATGACACTCTTATGTCGAATACATATCTCTGATAGCCAAACTGAAATATAATCTGATCTT
TGAGCGCTTAAGATCTGGTACTGTTGTTGTTGTTGATGATGATGATGATGATGATGATGATG
CCGACGCTCAATTTGGAGGATCGGTACTTCAAGTTATGCTAATGATGATGATGATGATGATG
GATTCATATCCTTTAGTCAAGAAACAAATTTTAAACACCAATATTTGGAATGATTTTA
CCCTTTTATGAGATACCTTCCAAATAGCGCAACAAAGGAAAGAGCTCTGCTGCTTTTGGCA
TGGAAGAAACCTTTGTTGATGAGAAATGCGCAATAACAGTGGGGGTACGCGCAATATTT
TTTTATTTATGCTGCGCGCTTATTTTAAATTTAGTACCATTATTCAGCTTATTTGTTCTTCTGTA

>YMR110C, 532 aa (SEQ ID NO 312)

MSNDGSKILNTPYVSKIDEIVEISRNPFKQLKSHENNRKXDLBFRQLQKLKLYYAV
KDHHEELIDAMYKDFHRNKIESVLNETTKLMNDLHLIELPKLIKPRRVSDSSPPFMFG
KTIVKISRSVLIAPNFPFLLAFAPLAAALAGNTIVLKPSELTPHTAVVVMENLLTT

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ACGGCTGAATGCTTTTGTGACCAATTACGGAGCGCTTAAGAGCGGACGCGCTGGAAACGG
CTCCATCTCTAAATCGGGAGGAGAACTCCGATACACCGCAGCATGGCAATATAGTGA
CAGTAGATGCTACACGCCCCCAATAATTTACAGTAGATCATCAACAGTCTCTCTCATTT
TCGGAAATACAGCAACTTCGAGGATTTAACTCTCAAGCAGTTAGCTCCGGAAC
ACGGTGATCATCTTTGACAGCAATAATATAAGCAGGAGAACTGCTCTACCTAGAG
CTAGAATAGCCATTAACCTATGTAACATTTCTACAGATCAATCAAAAACAATCTCAAT
CACAGAAAAATAAAGGCATCTGACAGAGAACAAAGCAGCGCAACACCGCTTTTG
AGAACCTTAGGCATCGATTTCCGAGGAGTGTATCTCTGAAACAACGATCAGA
GCGCCACTCGCATGATATGCAAAATATATCTCTCGGGCAAAACAACGATATA
TTTACATCGCGCTCAAAATTTTGAAGGATGATTTGTTCGAGGATCTCGGTGATCTC
TGAATCCGGTTTAGCCCCCGGCGAGTCCATAATTCGCAATCTCTGCTCCACTAGAC
TTTCCGGTTTTCCTCTACTAGTTTGTCTATCCATGTTCAATGCAAGACGATCAAGCA
TCACTATCCCTATGTTGTTGGTGTGGTGCATGTTTACGGTGGCTCGTTCACCTCA
TTGCTGATATTTGGAATTCCTTTAGAGAACATTTTCGGTGTGACAGCCCTGTGTTCT
TCGGCGTTTGTGTTAGCTTCGGTGTATATACATCCCTTGGTTTGGAAATCTAGATG
CCTATAAGCAACAAGAAATCCGACCTTGAAATGCGCTAGGTTTATCTCTAGGATGGG
CACTCTTCACTTCGGTCTTCGCTGCGCATCAATGAAATCAACTAAATGTTTTCCT
TATCTTCTCTTAGCAGTACCTTTTACTTCTATCCATTTGCAAACTTCACAGCGGAAG
TTGGCGTCACTAGAGCTGGTGGGCTCTTGTGTGATAGCTTCAATTCGCTGTGACA
ACGCTTACGAGGTATTCGCAACAAGACAAACCTCGTACATATGTTCCATCCCATTCGAT
TACCTAGCAATGATAAGGTGTTCTCTTAA

>YNR002C, 282 aa (SEQ ID NO 340)

MSDRQSSGNATFNPALDSESEFTSENDDSRHSOESICKIYTAGKNARQIYIGROK
FLRDDLPFAPGGTLPGLAPAVNKHFPANPAPLGLSGFALTTFVLWSPNARQIITPNV
VCGMFGVLGVQIAGIWEIAWENTFALCSFGGFWLSFGAIYIPWFGILDAYKDKES
DLGNALGFYLLGWALFTFGLSVCTWKSIMFFALFFLLAFTFLLLSIANFTGEVGVTRAG
GVLGIVAFIAWVNAYAGIATRONSYIMVHPFALPSNDKVF

>YOL139C, 1142 bp, CDS: 501-1142 (SEQ ID NO 347)

ACAAGTTTGATCTGTTATGTGACTCTTGTGAAGAGAGATACATCTTGTGTTCTAT
GTGAAGACCATTAAGAAACCTACCATGTCATCTCCCTGTGGACAGAGGTCACCT
TCCAGTGCAATCAAGATGTTTCTCGATGAGATGAACAAGATGTCGCGCGGCTGCC
CCGGTGTGCAITCATCTAGTCTTCCACATTAATGATGATTTAAACATATCATCACCAT
GTTTAGTTAAATCGTTTAGAGTAATATTACCGTCAAAAGGTCGGGTAAATTTTATTA
CCCTCTCCGAAAAGAAAATTTTTCGTCTCAATAGAGTTTAAATGCAATPACCTGATATA
GAGAGTTTACATTTGCAAGAGTAGTGTAAATCTCGGATTTATTTGTACATATGTTGT
GTGTTAGTGTCTGATCTTCTTAGGAGTTTACGAAAATAAAGCAATTTTGTCTGAA
AACTAGTAAAGGAGAAAATGTCCTGTTGAAGAGTTAGCAAGAGTTTGAAGAAAACG
TTTCACTCGATGATPACCACTACTCCAAAGACTGTTTTAAGTGACAGTGTCTCACTCG
ATGTCAGCACCCATTGAACACCAATGACCTTTATGTTACAAAGCCAGCCGTCGATA
AATCTAGTGTGCTGTGATCTATACCTGCGCTCACTTCAATCCAACTGTTGAAGAT
TTTGGCTATCATTTCAAAATTTCTGAGCCACACGAACCTACCATTTGAATCATGATACC
ACGCTCTCCGTAATGAGTAAGTGTAGCTTAAGTGGAGATGAAGCAATTTAAAGGTGTA
AATGTTCTTCCAACTTAGGAAAAGGTGCTGATATGATGAATTTATGCTAGAAGCTT
TACTAGCAGTTATTTGTAACAAATGATGAAGACGACTCCCAAAATTAACGGTGTCTTT
THAGCATTAAGAAAGGTGTTACAAAGTTTTCCTTATGGATAAATCTGAAGACAAAGAC
CACTATTGAGAAATTTGGTGAATTTCAAGCAAGTTTAAATTTAAACGATGACGGGCAAT
TCGAATTTCTTCCACATTCGCAATGTCGAATGTCAGACACCCCTCAACCATCAATCACCTTGT
AA

>YOL139C, 213 aa (SEQ ID NO 348)

HSVEVSKFEEVSVDDTATPKTVLSDSHFDVKNPLNTKWLNTKPAVDKSESWSID
LIRPVTSTQVEEFVETIQLPEPHELPLKSDYHVRNDRPWEDEANAKGKWSQLR
KKGADIDELWRLTLAVIGETIDEDDSQINGVLISIRKGNKFPALWTKSEDKPELLRIG
KPKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

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>YOR120W, 1439 bp, CDS: 501-1439 (SEQ ID NO 353)
TGTCTTACATATTTGCAATGATATGCTTGGTGATGATCTTCTCGGCTTTAGATATTTG
AAACTTAACTCTTGTCAACAACTTCTCTATGAGTGTATAGAAATTTGTAGTTTATACAC
CGCGCAAAATCGGGCAGACATTTCCGGGGAAGAACAAAGGAAGGGCGCTTTTCTTCC
TCAATGCTATAGCAAGGTCAATTTCCCTTCTAGAAAGGGGTAGAAATCATCTAGACAGC
AGATTGCAAAACGGCTTAATAATGCTATACGGCATTCACCGTGTGACGAATCGCA
CACCGTGTCTCTTAAATTTCCCTAGAGTAGAAACCGGAGCTTTTCAAGAAAAGACTACGGC
AGTAAAGAAATGCTTTTACGGCTATATAAACCGGAGAAATCAAGACATTTCTAATGACTT
GATTAAGATAGAGCTTAAATAGGTGCACTTTAGCAAGCTAAATTTTGGACAGCTTCAT
TACTAAATTAAGATAGAAAATGCTGCTACTTTTACATGATTTCTAGAAAATCTCTTCTC
TAAATCTGGAGCCCAATCTCTCAATAGGTTTAGGTAGCTGTTGGCAGTGCAGAAAGAACG
ATGCTTATAGGCTGTTTAAACCGCTTTTGAAGATGGCTACCGCACATTTGATCTGCTG
CTAATTAACCTTAATGAAGCAAGAGTGGTCAAGCATCAAGATTTCAAGTTTCTCTCGG
AAGAAATCTTTGTTTACAAAGTATGTTGTACACAAACACCAAGAACTGGAAGACTGGC
TGATCAATCACTAAAGAGGTTAGGATTTGGACTAGTAGACTTATATTTGATGCTATGGC
CTGCCAGATTAGATCAGCTTACATCAAAATGAAGACATCTTTGAGTGTGCCAACAAAGA
AGATGGTCTCTGCTGAGTGTATCAACATTTGGAATTTTCAATCAAACTGGGAATTA
TGCAGGAACCTACCAAGACTGGTAAACTAAGGCGTTGGAGTCTCAACTTTTCTATAA
ATPACTGAAAGATCTATTAGATCTCAAGGTATAAGCTTAGCCGACGCTCTAACCAAG
TCGAAATACATCTTACTTCTCAAGACGAATTTGATTAATTTTGTAAAAGTAAAGGCA
TTTGTCTTGAAGCTTATTTCTCCGTTAGGTAGTACCGTCTCCACTTATTTGAAGGAACCG
TTTATCTTGAATTTGCAAGAAAATTAACGTTTCAACCGGACACGCTTGTATTAGTCTGG
ACGTCCAAAGAGGTTATTTGTTGTTGCCAAAATCTGTAATCCCGATCGAATCAAAACGA
ACAGGAAAATATTATCTTCTTACTAGGACTTTGAAGCTATCAATACATATCGAAGG
AAAAAGGCGCAAAAAGGGTTGTATCTCAATTTGCTCTCTTTTCGAAATATTCAAGTAA

>YOR120W, 312 aa (SEQ ID NO 354)

MPATLHDSKILSLNTCAQIPQIGLGTWQSKENDAYKAVLTALKDGVRHIDTAALYRNE
QVQGAJKDSGPREELPVTKLWCTQHEPEVALDQSLKRLGLDYYVDLYLWHPARLDPA
YTKNEDILSVPTKKDGSRAVDITWNWFKTWELMQELPKTKAVGVSNFSINLKDLL
ASQGNKLTAAANQVEIHLPLPQDELINFKSKGIVVEAYSPIGSTDAPLKEPVILLEAK
KNVOPGHVVISHWQRYGVVLPKSVNPDRIKTNRIPTLSTEDFEAINNISKEKEKRV
VHPNWSPFVEFK

>YOR122C, 1090 bp, exon1 : 501-513, intron1: 514-722, exon2:
723-1090 (SEQ ID NO 357)

AGGAGAGAGGCTGCTGTTGACGAGAGAGGATGATAATGAGGAAGAGAAGAGAAG
AGGACCGGATGAAGAGAACGCTCTCGTCTAAGAAAATTTAAAGAGAGAGGAGCAGCAA
TGTCAGAGAGAGGAGAGAGAGAAAAGATAGGAGCGAGACAAAAGAAAGAGGGTTG
CGGTATCGAGGACGAGAGACGAGGATTAGGAGAGCTTACTTTGTTTATATATATT
AGTATGTAACAATCGCAAGAAAATGGAGTGTACATGTTGTAGTATTTAGTATGAGGTTA
CTGTGTGGAGGTTTACCATGATTTTGGCGAGAACACGCCATGAAATGCTCTTTGTACG
AAACTATTACCCCATTAATAATTTTTTTTCTTTTAAAGCTCAGTTGACCTTTCTCAT
TCCCTCTTTAAACAACCTGTGATCTTGAAGAAAGATATAATTACATACACATAATAA
CCCACTACGATCGCAAAATTAATGCTTTGGCAAGGTAATGTAAGCAGCAATATCAATTT
TTTAAAGAAATAGTTCGGAGTGTGTTGTGACATGTTTTCGCAATGCCCCGATTT
TTGTGATCGCGTAAATTTTCAAGATTAACCACTCAGAGTAAATTTACTAACTGGAATATC
AAAAACATATGAAATTTTCAACATGAAATTTCTTCCGTTTTTTTCTCTACTTTTAAAC
AGCATACATGATAACTTAATAGGAACCGGTAAAGTGCACAAAAGCTGTCTACTCGAG
ACGAGTGCAGCTGTTTGGCTACTTCTGTTGGCTATCTTTTGAACAAACGAAATTTGG
TGAAATTTTCAAGGCTTCGCAATTCAGCTGGTTTGCAGAAAGCAATGGTTTGCATATTC
AGGCCAAAAGTTTCACTGTGTGTGAGAGCTGACATAGAGTATCTACGGGTAGACATGATGC
TGAGGCTGTTTGTGTGAAGACTAAGCAAAACCTGTTATTTATTTGCTCATTTATCCCAAC
CGTACAAAGCGGTGAGGCCCAAGATTGTCGCAATTTGGCTGACTACTTTGATTGATTG
TCAATACTAA

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AACTGCTAGTAACTATGATTAAGCTTTTGGCTTCCTATTAACAACAGCGCAAGA
TATAAGGAATAGTTGGCGCAAGTTTCAAGATTTCCAAAGAGCAATCCCAT
ACAGAACTGAAACCGCTTCAAAATTTCTGAACCGCAGTTGCGAGGATATCT
GTATACCCCGTTCAAGCTCAAGAGCTAGACAAATGACGATACGCCGCTCT
TACATAGGGCTGTATCTCTCTGCTGGAGCTGGAAGTCCGATCCCAA
TGTAGAGATCTTGGCTTAAAGTCTTCTTCAACGAACTGAAGTACGCGC
GGTTTGTGAAATCAATAAGCTAATATGTTGGCGCTCCACAGGACCTCTCC
AACTCGAATGTATGACAGATGATTTACAGGCTCTCGCAAAATCGCAT
CGCTTTGTGCGCCCTGTTAAGCTTAACTATCAATTTCTCTGCCACTTACG
AAGACGAGTCACTTGGCCACTTGGGAACCTGTGGAATACCGTCCGGA
CAATGCGAATATCATCTCTCTGACTATCTCTTGGCTTTTCCCAAGAAC
CAGGACTCTCTGATGCTGCTGAATAGATGTTAGCCGAACCGCTCTGCT
GTCTTTTGTGATCTTCATCACTTTTGGCAGTAATCAGTACGATTAATCC
GTTTATCAAGTTTAAACAGATTTGATTTTAAAGTTTCCAAAGTTAA
TGGAGATTCAAAATTTTGGGTAAATGATTTATGCGTGAATTTGCAATGGA
TGGAGAAATGCGCAATATGTTAAGGCGGAGATCTGCTTATTGGAA
TATATAAAGTACTTATTGAAAGGCGGACAAAGTATTAAATTTCCAAATAG
TAATACCAATTTTGTCTCCAGAGGACTCTCGGATTAATGCCCTCTGA
AACTCATTCAGATAATTTTAAATTTCCACATTTTGAATTTGAA
GATTTGGTGAAGTACGATCTTTACGAATCTGCCATATTAGAGCGCTCA
AGATCTTGTCTCGAGCGAGTGCAGAGACCGTTGGTGATCTTCTAGTAG
CCGCTCGGGAAGAGACCTTTAGTGATCGAATTTTAAAGTAATATCA
ATGTTGTTTATGATAGTAGGTTTCTTAAATTTGCCATTTGAAATAATCC
ACAGGATATCTGATCTTGCAGAAAGAAATTTTCAGCTGTGGGTAATA
GAGTGAATTAATCAAGAGGATGACCAATGGCAATCAAGAGCGG
TCGGAAGAGGATTTAGATAGATCTGTGATAGTGAATCAAGCTGCGGCTC
GTTCTGCTGCAATGAATTTATCCAGAAATCTCTCTGCTATTGAAAT
ATCATTTCCCAATGACAAATTTTCATACCGAGGTCTACTTTCATAC
ATAGACCAATTTGTCACATTAATTTTACCAAAATCTCTCAAAACAA
TCGCTTTTGGAGCGGCTGGATAGTCCATAGAGTCCATACATCTAT
TATCTCAAGGTAAATGAAGTGTGGCGTTCGAGCATCCCATGGCCCA
AAAGATCTGCTCCAGAGCAAGATGATTTACAGTTGAATTTCTCAAG
TCAATTAATGATTTGAAGTAAAGACCGCGGCAATCCATGGCTTTA
TCGGATTTCTCGGCAACTTATATACATATATTCTTGTCTCAACTTTG
CCCAATGACAGCAGCTCGTTTAAATTTTAGCGAAGAAACCTGTATGA
TACCAGACGAGAGAAATCTAATCAAGAAATGTGACCATACACCAATA
TGACCTGTGCTCCCAATTAATCTTCTTGTGATGCTCGGATACATCTTT
ATAGATGACTCCGAACTTCTGCTGATGCTTCGGAATACATCCGATAC
AGAACAAGATTTGATAGATGATGCTTTGGAGATTTTCATATACCTTA
TGTGTCAATTTACACTTCGCGGTAACTGCTGCAAGCATGACTATCCG
AGTCTATAGTTACAGATGACACTTAAATCTTAGCCCAATATCGACATTA
TTCAGGACTACCAATCAAGCTAGATAATCAATTTGATCTTGCACCAAG
ACATTTAAACGAAGAGAGACAGGATTTCTTATCAATCTAGAAACTGGT
TGGCAAGCGTCAAGATATTACGAGCTACAGGAAACCGCCAAACCGGA
CCATTTAGATTTCTATCAATAGCTTATGTTGATCTCAAAATCTACTAAG
CGCTTGAACCTCTAAGCAATGCCAAGCGACGAGACCTCGAGGAGAT
GTTCCAGAACTCTGATGATGATCAAGATGATGTTTCCACGCTACATAA
TGTCTGTGCGAGAGCCCTTTTCCCTGCTCTGTGA

YBR133C, 827 aa (SEQ ID NO 54)

MHSNVFVGKPGFNHKKHRSKRSFLENVSSHSPFLPSNYDYVLLPTTPR
YKEIVQVFPKDFQRQSQIQNWKPQIQPEPQLQDICI PPFNVKKLNDNDTPS
YIGLLSWMLESRDPNVRDGLKVLNCKYARFVGNKLILAPPRDLS
NLQYLQMIYRLQNRIVFAAPALITISLPLXEDSDPLATWELNWTVRK
QCEYHPSLTISALPRTPTSVLNRMLAEPVSCILLVSSSIFASNQDYDP
VLHKNQNLILKFKVNGDSQSLGNELCVILHGMKEYANNVKGESAYLE

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YINYLKKGDKVLNSNSHQFLQEDSRIMPPLKPHSDNLNLNSTYLTFEK
DLVKYDLYESAILEALQDLAPRASAKRPLVILVACAGRGPLVDRTEFKIIS
MLFMDSKVSIIEKNQAYLYLQKRNFDWMDNRVKLIKEDMTWKQINEP
SEKRIQIDLICISELLSGFCNLSPECLWSIEKHYSHNDTIPIPRSYSSY
IAPISPLFYQKLSQTRSLSEAPWIVHRPYCIISSRVNEVWRFEHPMAQ
KDTVQDEDDPTVFESQSSLSNEFKIKHRGEIHGPIGPPSANLYNNIPLSTL
PNDSTVRLKPSSEETLMNTRREENLIKDKDTPNMTWSPIIPPLKQPISF
IDDSLSVLMSRLHSDTEQKVVWBSLESFIYLMLSNYTSVATAASMTIP
RSIVTDDTKTLAHRHRYSATNTNQDLNDQDIDQDIENEEOGGFLSNLETG
RSVQDIGHLSETAKPDHLDLSINKPMFDLKSTKALEPSNELPRHDELED
VPEVHVRVKTSTVSLHNVCGRAPLSPL

YBL085W, 3443 bp, CDS: 501-3443 (SEQ ID NO 31)
AAAGGGAAGTATGCGATCGCTAGAAATCTTTCTGGAACACTTGAAGCAT
ATCATATAATTTGATGAACCTTGTCTTCAAAAGATGTTACCAATATTCA
ACAGATATGTGAGCTTCTTATTTGATGACGCTAAGAAAGGCTATCACGT
GTGGGGGAGAGCTCAGCCACATTGCACTACTTTTCGAAACCGCTAGTTC
GGAAACGACATTCCTCCGCTACCAAAACAAACGAAAGGACGTGAAAGGTAA
ATGAATAACATGCGACATAAAATTTGGCAGAAACGAAAAAAGAGGAA
AAAGAAACTGAAACATACTACGCTTCCCTTTAGGATACTTTCTGATTTACAT
CGTAAGAAATTTGGGTGCGTCAATTAAGGCAATTTCTCCCTATATCAAGCA
GTTTACTGCTGCTGTCTAAAGAAACAAATGCTTTTACTGAAATTTCAACAA
AGTTTACTGCTGAGGTGACCGGAGGCCACTGTATAATAAANAATAGNAAG
ATGAGTCTCGAAGAAATACCTTAGGCAAAAGGGCCAAATCTTTCTCTCT
GTATTTGCGGTAAATCAGTACTCTTAAACGAATGGAGACGAGCTCAATA
TGAAACACAGTGATATAATTTAAAGTACTTACTGATGATGGGAGTACAAAT
GACGGCTGGTATTATGGGCGCAATTTGAGAACCAAGAGGAAAGGTTTATA
CCCAGCGTATTACCAAAAGATAGCAATAGAAAACCAAGAGAACCTGCG
ACAAATACCCCAAGAGGTGGAATTTCTGGTGTAAATATATGGAAAT
TTAAATGATTTCTGGAGTAACTAGGTAAAGTCTCTCTCGCATCAACAGGA
GAAAGAGCTAAGAGTGGTTCAGTTGAACAAGAGGTATCAAAAATCGCCC
GAAAGATATACATTTGAAAGTACAAATGACGATATAGACAAAGCCT
TGAAGAGCTAAGAGTGGTTCAGTTGAACAAGAGGTATCAAAAATCGCCC
ACACGCTGCTCGAAGTTCAGCTCCACAGTTGCAAGATGAACAGACTTT
TTTCTAGCACAGCGGATTTAAACTTAAAGTTCTGATTTTGAAGATATTA
AGTAAGTCAAAATATCAACAAATCCCTAGAACCGAGTTCGGAAATCAGT
TCGCTAAATTAGATTTGAAATTTGCGTAAAGTTGGAGCCCAAGAGGTTTA
CTGATTTACTTTAGCTTGGTGGATTTGATCAATCCACTTGGCAATAAATTC
AAAGAGCATCAAGTCTCCGAAATAATCTACTGGAATTAGAACTGGAACA
CCTAAAGAAATTTGAAATAAAATCTTTTGGTATAGATTTTCAGATATTCA
AAGAAATAAGGAACATCAAGTTCGAATTTGATTTGCTGCTCAAAATAACTG
GAGCGGACTACTCTACCTTTGCTTTTGAACCAACCAAGCTGCCCACTAAT
GCCTGAGCCACTGTAATAGAGAGCAATCCAAACAAATAATTTCTCCCA
AGTGTAAACAAGTTTCAAGTGAAGCTCTGATAGAAATCATCTCTCGGTC
ACCCAGAAATTTGCAAGACCAAGCTCGGTGTTGTTAATCCCAATTTTAA
AGTCTCAGACCCAGACTGAGCAGATCTAGATATGACAGAGTTCCTAAAT
TGTTTGTCTGATAAAGATTTTTCGAATCCCGGGAAGGCTCCAAACCA
CCATCATATCCAAAGTCCAGTTCAACCTCCACAAATCGCCCTCTTTTAAATA
CAGGTACACAAATAATAACGCAAGTTTCTCTCTCAAAACAAATATCCAC
CTAAACCAAGAACCCCAACCGTTTATTTCAATGGGCTAAATTTCCAAATCT
TCGACATCTTCCGATTAATCAACGGGCAAGTTCAAAATCTCTCGCATGA
TGGTCTATGACTCGAACTCTTAGGAAACCAACACTGACATCTGCTACTATAC
CTTCTATTAAACCGGTTAACCATGAATCTCTTACCCGCAATTTCCAAAT
ATATCTTCAAAATGCTACATCTCATATCCGGAACAGAAATTCGCTGTTGTTA
CAATAACCAATAAGAGGACGGAATCCGGAAGCTCATTTGTGATTTGTTCA
ACAGGATTTCAATGCTATCGCCAGTCAAGTCAAGTTTCGACGCAAGAGAA

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ACGAAACAACCTTCAAAAGCTAGACAGACGATTTTGAATCAGCAGACGAG
AAAGTCCTTACAGACATTCGAAGATGACCTTCTGAAATGCAAA
AGCATAGGAGAACTCTTATATATCTTTTCTTCAAAATGACAG
TCTATATCCACGTCACCAACCAAACTTTCATCTGATCCCGAAA
GATGATCTCCCATCTCGTCTCAGTCGAATTCCTATTCGCAATGCAAGAT
CAGATCTTACCTCCATAGTAGAATAACACTGCTTATGTTACGAGCCCTTG
AAAACCTCTTAAAGCCCTTAAATTCCAAATCCGAATTCGTTGATACACCAA
TAGGAACTCTCTAGTAGATATATATAGAGGAGAGATTCACACCAA
GTGAGGAGAGACAAACACACAGACACAAAGACAGACAAACAC
AAGAACAATGACCAAAAGATTCATTTAGAGAAAGCAAGAAATCTAAA
ATTATTTAGTAGACCAAAAGATTCATTTAGAGAAAGCAAGAAATCTAAA
GATCTCCAGATGACTTACCAAAATCTGCAAAATGATCTTCCAGAG
TCGAATGCTAAAAAGCAACAAACATCGCTTTTACGAAAGATATGCTTC
TATCAGACGAAAGAAATCTATGCAAACTGCGGACTGTTACAGGCTGATGA
GCAAAAGAGTACCGGCTCTATGAGGACTTGGAACAACAGCTTTTTCACA
CTTCATGGAACAAGGCTTCTTATTTTACGAATACCAATGATGAGAGAG
GCGTGGCTGATGATATTAACGGACATAGGGCTTACCTGCAAGTATG
ATGATAGGCTCATTTCTTATACCTGCGAGCTTAAAGAAAGGAAATACCT
TCTTTCAATTTGGTCCCTCCGCAACGGGGTCCAAAAGGGGCTAACCTT
TACAGAACCTTCGGCTTCTATTTGCAAGTTGAGATTAATCTGAAATGA
AGCATGCGCTGACGCAATTAAGGCACTATGATATGATACAGAC
GTCCCTGATATGATTCATATGCAACACCAAGATCTTATGAGAGAC
ACAGACGCTATTTGGAAGATGATCAAAACCAAGTATGAGATGCTG
AAGAGAGAGGAGAGATCAATTTGATGAGATGACACCAAAATATAA
AGAAATCTTAATTAATCAATGCAACAGATCAATTTGAGACCAAGGATTA
CTGGAAGTTCAGACATTTGAATACCTGCTGAGACACTTTTA

YBI085W, 980 aa (SEQ ID NO 32)

MSLEGMTLKGAKSPFLYIAVNOYSKRMEDELNMRGDKIKVITDDEYN
DGMYYGNLTKKEBGLPYAVTTRKAIKREPELHKSPQESGNSGYKGN
LNDASNIUKVSSHQENRYTSLKSTMSIDIALLELRSGSVEQVSKSP
TRVPEVSTPQLQDEQTLQEKTRNENTHDSLFSTDLNLSSESLKNT
SKNSISTKLEPSSSESVRLDKMAKSWSPPEVTDYFLVGFPGQSTCNK
KEHQVSKLLELEHLKELEINSPGIRFQLEKIRNIKSAIDSSSNKL
DAVSTFAFENQAOLMPAATVNDEIQQOISCKNKLSESSDRKSSSV
TTBELQRPSSVVNPNFKIHDPAEQILDMTEVPLFADKDFESRGAAPK
PSYSPVQPPQSPSPNNRYTNNNARPPQYTYPPKKNKPTVYNGLLPNS
STSDNSTGKRFKPFAMNGHDSNRKTLTSATIPSIINTVTDLSLPAISN
ISSNATSHHPNNNSVYNNHKTSGSSFYDLFNRLSMLSPKSSPDEBE
TKQPSKASRAVFDASARRSSYGRSDASLSEMKHRNSSLFSFSKSO
SNPSPPTQUTPIDPAKMTSHSRQSNYSHASQSYSHSRKHSIYVSP
KTSLSPIKSNKINIALAHSEPTSSNNKEAVSOPSEGRHKHKKHRSKH
KNSSSKDSSSEKSKKLFSTYESFVSGKEFRSPSELQKSTKSLLEPR
SNAKQOISAFTEGIRISITAKESMOTADCSGMSKGTGAMTWKQRFPT
LHGTRLSTYTNDEXERGLIDITAHVLPASDDRLISLYAASLGKXY
CFKLVPPPGSKKGLFTEPRVHFAVENKSEMAWLSAIIKATIDIDS
VPIVSSVATPTIPLSKAQTLEEARLQTLRDABEEBRDQPMDDDTQNK
RNSNVPIDODQFETSDYLESSAFEYPPGRIL

YDR545W, 5891 bp, CDS: 501-5891 (SEQ ID NO 137)

TTCTATTTATTTGGCTTTTTCGAGAGCGGAAGAGTTGTAGGCTAGCGC
AGCGTAAGCGTAGCTCATATTTAAAGTATCCAGAAGATATCCAGAAG
CGGTGAGCAACGACAGAAATCCGTGTTCTCTCGACTAGCAGATAGT
AAGATACGTGACCATGGAATGGAATAACGAAGTACGATCCGACTACT
TTATTTTGCAGGCCCGGAATCAAGCGATGATGACATCTTCTGTTT
TCTATGTTGGACAGACAGTCGCTTATCTTAGTGAGATTTCTTATTAAC

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GAAATTTCTTTCGCTGCTGCTGAGATTGCACTGCAATAGCGCAGATTCT
GCTTCTTCAATAGAGTACCTTAATTAATTAATCTTAGATGATGATTA
GACGGAAGTCAATCTTTTATTTATTTGATGATGATTTCTTGTCAAAA
AGCATACAAATCAACATCTTATTTGTAATTTGGAACCTTACAAAATTA
ATGAAAGTTTCCGATAGGCGGTAACTTTGAAAAGCAAACTTTGACAGATT
TGAATGCGCTTAATTAACAAAAGACATGTTGATCTTACGAGACGAA
CTTATTTGATGATGATCCCAAGGAATGCGGTCAATCTACGAGACGAA
AAGTCGCGCTTAATCAAAAGTGTAAATGTCAGAACTGTGTGCAAGATG
GAAAAGGCTTTTGAATAAAATTTGTCATTTCCGTATGCTCGGGAATAATG
TACAAAAGTCCGACATTTGTTGTAAGACGAACCAAGTTCACAGGCGGA
CCATCCCTTCAAGTATCTTATTTCCCAAGAAATCAACTTCAATGCTGTA
CAGTTGTTTCAAGTATCTTGTAAATTTCAATGAAAGATTTAGATTA
CCCTTCTCTTTTACCTCAACAGAGATTAATTAAGATGATGATTTTC
CGTGTCCGGAAGCTGTGACGAAATAGCGAGTCCAGGCGACAGACAG
CTTACGATGCGTACTTTCAGTGAATTTGTTTCCGTGCGACCAATGTATA
GGAGTCTCAGAAAAGCACATTAAGAAATTTGGTACCAATTTGSCACCC
TACATGTTCTTGTATCTACAGCTAGATGAGCTATGATTTTCTTGCATTA
CCAAAGCAAGTTTACCTGCGGAAAAGAAAGTGCACACAGCGGCTGAAG
GTGATCTATGCTCCACGTAAACCAATGAGATTAAGTATTTTCAAGATTA
TGTACGATATGATGACAAAAGAACCGATTTGGTGTGATATTTTGCATTA
TATCTTGGAGCATATGCGGCTCAATTTGGGGCGGGTCCCGGTGTCGCG
CTGGTGCAGAGAGATGATCTATTAACAAATGAGAACCCATTTATCC
TCTGTGACAGCATATGCTGTGAAGTATGTAAGTCCGTAATTTTATCC
TCCAGAGACTCAGAAAACCTAGATGCGGTGAAGCTTTATTTGATGT
CGTTTGTGCTTGTATCGAAGAGATTTGATATTTATGATGACACACAC
GGCTGTGCAATGTGAATGATCAAAATTTCTGTACACAGATGAGCGCA
GGAAACCAAGCTGAGAACTCTTAATGAAATTAATCTTGTGATCTTCTGT
ATGGAATATCAATGATGTGGAATACTTTTAATTCGCAAGTATGTCGGGCG
TTTATCTTGTGATGCAAGGCTCAGTTCGATTAACCTTTGGGAGAGTTGAA
CACTGCTTTTATATGCTTACAGTGTGATATTTGCAAGCTATTTGAC
GTAATCGAAGATTTTGTTCAGAGACCAAGCGAGAAATTTGACAGTAT
CTGGAACAGATTTCTTTTCTTAATGATACCTGTTAAATATGCTGTAAT
TGTGCTGCCAAGTTGAGAGATACCTTACCTTATCAAGACCTTCAAT
AAATTAAGTCACTGTGCAATGAGATGAGCTTACCTTATCAAGACCTTCACT
ATGTCATATTTGCGGTGAGATACCTTACCTTATCAAGACCTTCACT
ACTGCTTTTCCCGGTCCAGCGCAACGTAATGCTGATATGCGAACAA
GACGATCCAACTGTACACTGATTAACAACAGAACGTTTATCGGAGCT
CGACTTAAAGACCTTGAACGATCACTTACAGATTAAGCTTATTTTGT
CACTGTGTAAGGCAATGCAATATGTCGCTTGTGTAACAGTTATGACG
CTTTATATCATGATCCTTGAATGATGAGATGAGTTTGTATTTCTACATCTT
CAAGTAACAAATCGAGACATTTGAGATATGTTTGTATTTCTACATCTT
TCTGAATACCGGGAAGGCTGCTGAGTGAATGCAACTTTTGGAGCT
ACATGAGGGAATCTCCGAGAAATGCACTTCAAGAGCTGAAATTTTCGGAG
ATGCGTCAGGGGTGATGCTGCTGAGAGCACTGCGATGAGATGAGATTA
TCAAAAGATTTGTACAGATGTCGCGAGAGATGAACTCAATGCCAATCAT
CGCTTCAACAGGCGCAATATTTACGTTGTGATCTTTTCTGTTAACT
AGTGTAGTGGAGCAACCGCACCTTATATGAGAAAGAGCTTCCGAGCG
CTGGAATCAATGTTAGGCTTGAAGGCACTCAATGTTGATTTCTTCTA
GTACTCGGAATCGGAAGAGTATGAGGAGTGAAGGCGGCGATTCAGAT
CATGATCAAAAATTTCAAGATGACGGAATAAGGCGCCGAGAGCCCAA
GATGACAAACGATATCTTCTGCGAGCGCAGAAACTCTTTGCGACAGCTCT
TTGAATTCAGGACTTGCATCAGTTGCGCTTATATGATGAAATTAATCATG
GCGACACACCTCTGTGCGAGTACAGGCCACCGGCTTAAAGGCGACGTGA
GGAATATTTCAATCTCCCTTATGACACTGCGCTTAAAGGCGACGTGA
AATATGTCGTTTCTGTTTATCCGTACACAGTGTGCTTCTTAAATTC
ATGATCAGGTTGAGCCGATGCGGTTGCTTGAATGTGCGCCCTGTAAAGAA

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CTTTATGTAAGAAGGTTCCGATGCGGCTTACTGATTTATAGCTGGGATCT
ACCATGATCTGCTAGCACTAATTTACAGACAGAGTAGCTGCTGGAG
AATATTGTTGAGTGACCTTTAGGACCAACAACGTAATAATTTGGTTACCT
CATTTAGATAGTTTACAACTTTGAAACGGAGGCTACCGCGACTGCG
AATTTGGGGGCAATAACCTTTGAGCGCTTTGAGAAAGCAATC
TTTTTGGCGGCACAGCACTGAGCTGAGCTGCTGCTGCTGAGCG
TATTTGGCTTACGGGACTGGCCAGAGTCGATGACATCAACAGGCTCA
AAGGTCGGGAAGATCTACGACAGAGTCTATCCAGCTATCCAAACAGGATG
TTTAAATCTAATCAAGGAGAAATCCGAGGTCTTTAGGGCATCTTCTATAA
TATCTGACTTGAAGAAATGACATTAAGCAATGATGATGATGATGATGAT
ACAACCAAGAGTGAAGAAATGCGCTCTCTTGGAGAAAGTATTTAG
GGTGTATGATGATCAAGGAAATGCGGCTGCTGCAAGAAAGGTTCTGCGCA
CAAGGAGTTGTCTACTACGAGCTAGCAAGTCTTCTATCGGAACGAAA
TTAGTACTTGAAGAAATGACATTAAGCAATGATGATGATGATGATGATG
TGATATAGACTTATATATATAGTCTATCAAGCGCTAGGAGACTAA
GAGATGGGCGCTCTGTTATCTATCTATCTAGAAATAACAGTTGGGGCA
AGAAATCGGAGGTGATTAACCAAGTAAAGGAGGCTGATTAACCGA
ACAGGTACGCGAGTTCTATGAGCTTGAATCAAGAAAGGAAAGGCGC
AGCATGTTGATGCTGCTGGCTCCAGGACAGACTGCTGCTGCTGACAGTG
GAACTGATAGAAAGATGACAGATGCTGTAATAACAGCGCAAGCTTC
CATGTCGATCAATGCGTTACCGTCTAGCTTCCAGGAGCAATAGCAGTG
ACAGGTGCGCAAGATGATGCGAGTATGAGGACAGCAGCAGCTGCAATG
CATGGTAGTCTANTGCGAGTACCAATGCGACTACCACTCCAGCACTAA
TGCTACTACCACTACCACTACCACTACCACTACCACTACCACTACCACT
CCAGCATCAAGCTCAGGACTAGTGGGATACCACTGAAGTACCACTCC
AGCATTAATGCTACTACCACTACCACTACCACTACCACTACCACTACCACT
TACCACCTCCAGCATCAAGCTCAGGACTAGTGGGACTACCACTGAAGTA
CCAACCTCAACACTAGTCTACTACCACTGAAAGTACCACTACCACT
AGTCTACTACCACTGAAAGTACCACTGAAAGTACCACTGCTACTACCACT
TGCTAGCACTCACTACCACTACCACTACCACTACCACTACCACTACCACT
CCAGCATANTGCACTACCACTGAAAGTACCACTGAAAGTACCACTGAAAG
GAGCCAAATAAGATGCGCATCTAGGATATAGATTTCCATGCTACCACTG
CGACATAAACAAGACTGATAGCGGAAAGGAGTCAAAATGGTTTTG
TAGAGAAAGAAATGAAAGCAATTTCCCAATCTCCGAGAAATG
AATGCTCTACAGTTCTTGGATTTGGCTGAGCAATTAACATCTTTT
CCTCTATGATTTGACGATATCTCTGCGGAGGAGGATTTCCACCAAT
ACGGATTATGCAAGGCTGTCAAAAGATGTTGAGCTCTGCTGCTGTTGG
GCTGGCCAGAAAGTATGTTATGCGAGGATGCTTGGGAAGCACTAGCTGT
CGAGAGAACTGCTGCAATGACGAGGAATACAAAGAACTTGGGAAGACA
TCGAGCCATACTATGCGGACCTTGAAGATATTTGAATAATTTATGCGGTA
AAAAGGGAGAGATCTACTCTCAGATACAGAGAAATTAATGCTTGGTACCT
GGCCATTTAGAGAGAGAGAAACATTTAGTGTATTTGGATTTGACAGAG
GCAAGCAAGGAGCAAGTTTTCGCACTGCTGGAAGGAGAGATCAAGAG
TTGATTTATAAGATTTGAGCACTTGGTGAATCGAAGCAGAGTGCT
CGAGTACTTTTGAATGCTGGAGGAGAAAGTGGCGGAGAAATGGGAGG
CAAAAGCAGATACGCTCTTTTGGAAAGGCTGAGAAAGTGGAGTTT
CAGCGTTTGGTTCCATGACAGCGCTGACCTGACGAGGTTCCGAGTACGT
CAAGCTGCAATGAGGAGCATGACAGTGTGGAGGAGCAGATATGAAT
TAAGCTAGGAAATGCACTTGGAGATCAGTCTGCGTGGAGGATACCCCA
TCTAAGTGGCGCATGAGCGGATCTGCTGCTGCTGATGAGGCTGT
CTCAATTAACAATTTTGGCAGAACTGGAATATCTTTTGGAGCAGATTT
CGAGGTGTGGTTTACCACTAGGCTTGAATTTGGCAAACTGTTGAAGTT
CTGCTGAGAGTAAACAGGAGTACCGCTGTACATGCTGATGAGGCT
TCACAAAGAGCTGATGAGATGATTTCCAGCAGGATGATTTGATATAA
TATTAATATGATAGATTCGAGCAGAGAGTTGGAGAGTGA

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YDR545W, 1796 aa (SEQ ID NO 138)
MKVSDRRKFEKANFDEFESALNNKNDLVHCPISITLFBESIPTEVRSPYEDE
KSGLIKVXFRFGAMDKRKSFKEKIVISVMGKNVQKFLTFVEDEPDFQGG
PIPSKYLIPKINLWYTLFQVHTLKENRKDYDTLSFLYLRNGYINELSF
RVLERCHEIASIRPNDSTMTFTDFVSGAPFVRSLOKSTIRKYGYNLAP
YNFLMLHVDLBSLFSAYQASLPQBEKKVDTEBLKRDLCPRKPIEIKYFSQI
CNDMMNKDRLGLDILHILRACALFGAGPRGGAGDEEDRSITNEEPIIP
SVDEHGLKVCKLRSPTPRRLRKTLDLDAKALLVSSCACTARDLDIFDDTN
GYAMWKIKILVHEVAQETTLKDSYRITLVPSSDGI SVCGKLFNREYVRG
FYFACKAQDFNLWGLNCPYMPVTVDIASILLNRREVLPREPKRIGIDEY
LENDSEFLQMPVKYREIVLPKLRDRDNTKMTAALKXKVTVAIDELTVPLMW
MVHFAVGYPYRYPELQLLAFAGPQRNVVDDTTRRIQLYTDYNNKSSSEP
RKTLTDLGLTSDYFVFTVLRQMGICALGNSYDAFNHDPMDVVGVEDPD
QVTNRDISRLVLSYMFNLTAQKCLVEYATFQYMRLELPKNAAPQKLNFRE
MRQGLTALGRHCVGSRFETDLYESATSELMANHSVQTGRNIYGVDSFSLT
SVSGTTATLLQERASERWQWLGLESYHCSFSSSTRNAEDVVAGEAASSD
HDQKISRVTKRPREPKSTNDILVAGQKLFSSFFRDLHQLRLCHEIYN
ADTPSVAQAPPGYKTELPFLPLIALASKGVYVSFLFVPYTVLLANC
MIRLSRCCGLNAPVRNFIEEGCDGVTDLVYGIYDDLASTNFTDRIAAWE
NIVECTFRNNVKLYLIVDBFNHFEVYRQSQFGGTTNLDPDFDAPEKAI
FLSGTAPEAVADAALQRIGLTAKKSPDINELARSEDLSRGLSSYPTRM
FNLIKESVPLGHVHKWKVKVESQPEEALKLLALFELIEPESKAIIVAS
TTNVEELACSWRKFRFVWIGHKGAEEKVSRTEKFEFTDGSRMVLIGTK
LVTEGIDIKQLAMVIMLNDRLNLIELIQGVGRURDGGGLCYLLSRKNSWAA
RNRKGLPPIKEGCTIEQVREFYGLESKGKGQHVCGCCSRTDLSADTV
ELIERMDRLAEKQATASMSIIALPSSFQESNSSDRCKYCSSDESDTCT
HGSANASTNATNSNTNATTAASNVTASITTTASINVTSAITESTNS
STNATTAASNVTASITTTASINVTASITTTASINVTASITTTASITTTASIT
SATTTESNTSATTTASITTTASITTTASITTTASITTTASITTTASITTTAS
DANKDGNEDNRFHPVTDINKESYKRGKQSVMLERKKLKAQFPNTSENM
NVLPQFGRSDEIKHLFDIVYFCPEGVTFQYGLCKGCKQKMFELCVCM
AGQKVSYYRMAWEALAVRMLRNDDEEYKEYLEDIEPYHGDVPVGLKYFSV
KRGEYLTQIRNYAWYLAITRRRETTISVLDSTRGKQGSQVFRMSGRQIKE
LYKVKWSNLRSEKTEVLYFLWDEKKCREWEAKDDTVFVEALEKVGVP
QLRSMSTAGLQGPQYKIQF SRHHRQLRSYRSLSGMHLRDLALGVTP
SKVPHTATFLSMLIGLFYNTFRQKLEYLEQISEVWLLPHWLDLANVEV
LAADNTRVPLVNLMAVHKELDSDVDVDFRFDIILLCRDSSREVEGE

YCR005C, 1883 bp, CDS: 501-1883 (SEQ ID NO 71)
AGAGTTGTTGCCACACATAAGCCGCTTTGGAGTGTGAACAAATCCGTC
CTTGGGTCTTCAATCAATGGCTTGGCGGTATCTCAAAAGAGCGCAACT
AATAGCGCGCACATTCGACGCAATTAATCCGGTGTGTCATCGACTAGGGCG
AAGAGGTCACGACCTATTTTCTTCGAGAAAAAANGTGTGACCTTTTCC
GTAGCTAGACGCTATCAGGCGCTCAGCAATGGAGGACACAGCGGAAAAA
CAATAACAAATGGTAAGCAATACCTTTTGAGCGTTACATTCGTATGAA
ATTGGTGACGTTAATCTAAGATAGTCTCTCTCAAAAGGCGCCATTAT
TCTCGACGTTGAGCGTATATAAGACTTAAAACTTGTGTTCTTTAGATAT
GGTGTTCCTTCTCATTAATTAAGTTTCAGGGAACAATATCAACACATATC
ATAACAGGTTCTCAAAACTTTTGTGTTTAAATAATACTAGTAAACAAAGAA
ATGACAGTTCTTATCTAAATTCAAACAGAAAATGTTGCATCATATTACA
ATCAAAATTCAGCCCAAGAAAAAGACTCAAAAGAGAGATTTAGCGAAATCT
ACCCCATCTCATCTCAAGATGTAAGGCAATTCGTTTAAAGACATGGCAAA
ACTAAATTTAGCGATGTTCTATTAGAACACAGGTATATGTTGTTATGAGAGG
TATTTCCAGGAGCGTATGGAAGGTTCCGTTTTCGACCCAGAGACGGTA
TTCGTTTCAGAGGTGTCGATCGGACATTTCAAAAGAGGCTTCCCAAG
GCAAAAGGAGGCTCACACCACTACCAAGAGCTCTCTTTTGGTTATTGCT

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AACTGCGAGGTTCCAACTCAAGCGCAAGTTGAAACCTTATTCAGGCGATC
TATATGCAAGATGCGAAGTACTAGTCAATGCTCACTTCTTATGATTAAT
TTACCAAGAGCTTACACCCATGCTCAATTCCTATTTGCTGATCAATC
CTTGAAAGGAGCTCAAGATTGGCTTAAGGCTTATGCTCAAGAAATTTCCA
AGCAAGATTATTTGAGATTATCTTTTGAAGATCACTAGACTGCGGGT
AAATGCGAGATTGCAAGTCAAAATTTATTCGTAATGTAATTCAAAGATG
CAAAATGGGTGAATGAGCCCAATGCGGATTTGCTGACTTGAATGACCTTAT
ACTGATTTGGTTCTAAGATGAAATTTGCTGACTTGAATGACCTTAT
TTAACCTTATCTGGATCAGAGAGTGTAAATGATTCACATCATC
CCATCTTGTGGCTCAGCATATTCATCCTTATCTGCTCCCTGCTGACG
GTTTGAAGCGGTTGGCTGGCCACTTCACTGAGGCTTATCTAAGAAAT
CTGAATGGTTATTTGCACTTAAAGAGATTAATGATGATCACTACTTA
AGATACGATCGAAAAATATTTATNGGATCTTAAAGAAAACTGATCTGTTATG
TTCCCGGTTATGCTGCTGCTGCTAAGAAAACTGATCTGCTGTTATG
GCTCAGGCTAAGTTGGCATGACGACATTTCCAGATTATGATTAATGCA
GTTAGTTTCATCAATATAGAGATGACACCTGGCGTTATGACGAAACATG
GTAACATTAATAATCCATGCGCAATGATGATCTCCTGCTGCTTAT
TTACATATTTATGACTTAAAGATCTTCTTCTATACCGTTTATTTGG
CGTTCAAGGCACTTGGTATCTCTGCTCAATGATCAGTATGAGGCA
TCGGTGTCTTCCATTGAAGGCCAAAGTCTTATCTTACTGAGAAATACAG
GAATTTGTCAAAACATTGAACCAACTATAG

YCR005C, 460 aa (SEQ ID NO 72)

MTVPYLSNRNVAASYIQSNSQEKTLKERSEYPIHAQDVRFQVKEHGK
TKISDVLLEQVGMGRIPGSVWEGSVLDEPDEGRFRGRTIADIQKDLPK
AKGSSQPLPEALFWLLTGEVPTQAVENLSADLMRSRSLSHVYOLDND
LPKDHPMAQFSIAVTALBESKFAVAQGISKQDVMSTYFEDSLDLGLG
KLPIVIAKIYRVFQDKGGEVDPMADYAKNLVNLISKDEDFIDMLNLY
LTIHSDHEGANSATSHLVGSLSPYLSLASLNGLAGPLHGRANDEV
LEWLFALKEVNDYSDKTIEXYIMDLTNSGRVIRGYGHAVALRTDPTVM
AQRKAMDFPDELFRKLVSSIEVAPGVLEHGTKNPWNVDASHVL
LOYVGLKESFPYVLFQVSRFGLAQILTDRAIGASIERPSYSTERYK
ELVKNIESKL

YOL126C, 1772 bp, CDS: 501-1772 (SEQ ID NO 345)

ATCCCTCACTCTTCCGTTTGATCCCTACTTCTTACTCTCTTTT
TTCTCTTATTTGCTTGTGTTTACATTTGAATGCTATTTACTAGACAC
AATAGCTAGTCAATCCCTATCTCCGTTGCTCACTTTTTCATAATTTCT
CATCTATATAGCGAAGTACGAAAAAGATGATCTGCGGCACTCGGCC
TTCCCGGCGCAATGACTCATATCTACGATACGCGCCCTTAAATCCGC
AATTACTTTGCCCATTCGCGCGTACCGTTCTAAAGCGCGCGCTTGC
CCCATATCTCCCTCATATGATCCGGAGATTCGCGTTTCTTCTTGT
TAGTGCCATTTTGTGTTGCCAAGGTGGGAAGTCCGATTTGACTTTAA
GGAATCTACGGAAGTATCTAGGTTCTTAAATAACATATACAGCGCGTG
CGTAGATATATTAAGATTAAGATTTATGATATGATTAAGATTAAGTCTG
ANGATTTCCCTCTGATCTTTTCTCTGATATATTTTCTCCCTCTG
TATTAATTCGTACAGTACAGATGATGCTGAAATATGCTGAGACATAT
ACAAAGTTCAATACAAATATCAATAAAGTTATATGATTAAGTCTACTCA
GTTACCACTATCATAGAAAGATTCGTTAAATATGCCATTTTATGATG
TGC CGGTTGATCGGGAGTCTGTTATCGCTGCTTTGAAAGCTCAGTTGC
AATACCACTTAAAGAGAGCAACCGGAGCTTACCAATTCATCTGAGCT
CTTTAGCATGTCACCAAGAACCATCAAGGCTTACCGCGCACTTGTG
TCAATATGACACCCCATTTTCCGTGTCAGCCACCTCCGCGAGGAGCA
TTAGAACTGTTTGCATTAACGCTTCTATTTGTTGCTATCTTCCGAGGTT
CCAAAGAAAACCTGGCATGACTGCTGATGACTTATTTAACTGATAGCTG
TATCATTTAGCAGCTCGGTGATTTCTATTTGCAAGATGTTGATCTTTCCA

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AGGCTTCGCTTCTGTCATTTCCAACTCCCTGTATATTTCTTTAGTCCAGTG
ATGCTTTCTTAACATTTCTTAAGAACCATCTCTAGTCTTAAGAAATTCGGCAT
TGAAAGAGAGATAGGTGTCACCAAGCTGACATGTCAGAGCTGCCA
CTTTCTACGTGATTAACATTTAGTCTAGGGCTACTCTCGTGTATAC
TCCATCTGAGCTCCCTGTATATGGCGGGCACTTGGCGAGACTATAT
TCCCTGTTTTCACAGTCAACTCTCTATGAGAATTAATAGAGATCAAT
TGAATATTTAATATCATGCTCAATACGATGCTGATGAGTGAAGTGTCAAG
GCCAAGAACGGTAAAGTATGCTCACTTATGATGCGGCTGATGCGGTTA
TAAGTGTGTTGCCAATTTGTTCTTTGTTTATTTGGTACATTAAGCAGA
TCCATGGAACCTACTATGTCGATTAAGATGCAAGCACTTCCCAT
GCTCCTGGGCGAGATCAATTTATGCTCTGTGTGAGGCTGCACTACTT
TGCCATACCATTAATTTACTAAGAAAGGCTTCTCTATGATGATTTAT
ACATGCTTAATAGATGAACGATGAGAACGCAACCAATGTTGCCAAT
TGCCTCCCACTTAAGAAAAATATGATTAAGGGCTTGGAAATTCGTTGC
ATGAGATCTGCATCATCTTAA

YOL126C, 423 aa (SEQ ID NO 346)

MILLILIPCIYFLPFCINRWRSPEYSAADYKSSIOYHKSYSNMPS
VPSIEDPSLKIALILGAAAGIGQSLSLLAQLOYLKESNRSVTHILA
LYDVNGEAINGVADLSHIDTPISVSHSPAGIENCLHNASIVIPAGV
PKPGMTBDLFRVNAIGIISQLDLSIACEDLSKVFVLVINPWNVLVYV
MISNLKHNHQSNSGIERRIMGVTKLDIVASTFLREINIESEGLPRN
SMPDVFIQGHSETIIPLEFSQSNFLSLNEDQLKYLHRYQVGGDEVYK
ANNGVSATLSMAHAGYKCVQFVSLGNIEQIHGTYVPLKDMNFI
AAGAQQLPLVLDGADYFALPLITTTKGVSYVDYDINRMDEMRQMLPI
CVSQLKNIIDKGLFVARSASS

YBR019C, 2600 bp, CDS: 501-2600 (SEQ ID NO 39)

ATCGCTTCGCTGATTTATTAATCCCGAAGAAATPAGGCTAAAACTATGCGC
ATTATGATCTTATGCTTATATTTGATTTCTTATTTGAAGCTTTGTG
GGCCAGCTTACTCGCAATTTTCTCTCATACCAATTAAGCTAGTATTT
GAGAACTTTTATTTGTTGCGAGAGTGGCGGCGGAGACATCTGCTTT
CAGAAACGGGACCGGTGAAGACGAGACGACGAGGAGAGCTTCCGC
GGAGGCTGTGCGCCGCTCGCGGCTTAAATCCGATCTTCAATATTA
ATGACGATTAAGCGTATTAATCTGAAGTTCCAAAGATCAAGAGATTTAG
GCTPAGATTAATGGGCTCTTTTCAATTTCCACAACATATTAAGTAAGTTAG
ATATGATATGATATGAGGCTATGCTATGCGATGATATATGATTAATCTT
ATATGCTCATCAAAAATAAAGATTAAGATTTTGAATAATCAATATTA
ATACAGCTCATCAAGGAAAGTACTTCTTAAATTTGTTTGTGTAC
AAGGTGTGCTGATTAATGTTGTACACACTGTGTGATGAGCTTAATGAT
ATGATATGACTGTGATGCTGTGATTAACCTGTGATTAATCCCTTATGA
TCTGTATGCCAGGTTAGAGTCTTGACCAAGCATCACTATCCCTTATGA
GCTTGAATTTGTGACCGAAGAAAGTCTGAAAAAGTTTCAAGAAATATA
AAATTAATGCTGATTAATCACTTGTGCTGTTTAAAGGCTTAAGGTAAGT
ACAAATACCGCTGAGATATCAATATCAATTAATGAGTGAAGTGTGCT
TTTATTAAGCTTAATGCAACAATACAGCTTCCAAATTAATGATTTCT
CTTGTGCTACTGTATGATGATGCTACGAGATTCCTCAATATGATTTCT
ATCCCAAGAAATGCTCCCTTAGGCGCTAATATCGATATGATGATGAA
ATAGCGCATGAGATATCTTGAATGATCTTTTCAATGAGCAAAAAA
CTTGGAAGTTTGTCTATTCGCTTATTTTAAATCCCAATTTGTTGTGCT
TCTGATTAATTCGGAAGATCCGCTAGGTAATCAAAATTTGTTGTGCT
ATATATGAGCTCAATGATGCTTGTGATGAGGCGGAGAACTTATATCCAC
GAGAGCTTATATGATTCAGAGATGATGACCCGATCAAGGATTAATCCAC
CTACATGATTAAGCAAAAGTATGATTTGCAAGCCCTGCAATTAATGAGG
GTTCAATTAATAATGAGTTTGTGCTGATGATGAACTTGGGTTCCGGTA
AAGGTTTCACTGATTTTGAAGTTATATCATGATCTTCCAAAGCTTGTGCT

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ATTGATCTTCCATCAAAAGTTACGGCAGAGCAGGTCATCTTTTGAA
CTTGACCGCTTAAACAGATAGGGCCAAACCGCAACTGAAATGGCAGCCG
AGTTGACAGTTGAAGACTCTCGCAAGTTATATGGAATGGACTACTGAG
AATCTTTTGGTTACCAATTAAGGGGTGTCGAGGCCAGATTTTCCCGTGA
AGATATCGGTTATGACGCAAGATTTGTGACTATTTGTCGCGCCACAGAT
TTCAAGCACGTTTGGCCAAATTTGGGGCCAGCATTTGTGACCTGAAGTG
AACGCAAACTCAGTTTGTCTTGGCTATGAATAATGAGGAGGTTATTTGAA
TCTCTAGTGTCTTATATAGGGCCACAGATCCGCGAGGTATGCTAATCTGTA
TTTTCGAAGGGTAAGTTTGTATTTGCTATGCAACAAAGACTATCAGTTAAACCGTT
AATAACCGGCTTAATGCGAATCATAGTACTATCTGTTTTCACAGAAA
AAGATTTTGGGCCCATCATCTCAAAATCTTCAAAAGAGTTTTCACCG
CCAGTACATCTGATGATTAATGAGAGGACACCGAATTTCCAGGTGAT
CTAATTGTGAACCATACGCTAATCTGTAAGCTTTGCCCAAAAGTTTGA
AATGGTATATAAGAGTAATTAATCTGCTGGTGAAGCGACGCCAATAAAT
TAACAAATCATAGTTTATTTCAATCTGAACAAAGCCATATGAGACACTATT
GAGGTCAGGAGATTATGGTGGCTTCAAGCCCAAAATCCCGATTGATTTG
AAACATGATCTTACGGCTAATATCTGATAGAGAAATTTGCTACCTTTA
ACTTCAAAAGCCAAACGGCTTATAGGCCCAAAATCCCGATTGATTTG
TGTTTGTGGTGGATGAATCTGTAAGCTTTTCATCCGATTTCAATATTA
CAATGAATTGACGCTTATTTGCAAGCTTTTCATCCGATTTCAATATTA
CATTAGAGTTTATAGTACAGCCCACTTATCAATTTTATATACGGGTAT
TTCTGTCTGTCTGCTACGAGCAAGAGGTTTTCGAATTTAGCCCTGG
TAGATACATTTCTCATCAATCAAGAGAACTGGAAGATTGTGTACCT
TGA AAAACGGTAAACTTACGGGTCCAAGATTGTCTACAGATTTTCTCTGA

YBR019C, 699 aa (SEQ ID NO 40)

MTAQLQSESTSKIVLVTGGAGVIGSHTVVELIENGVDVADVADNLNSTYD
SVARLEVLTKHHIPFYEVDLDRKLEKVFKEYKIDSVIHFAGLKAVGES
TQPLRVYHNILGTVLLELMQVNVSKFVSSTATVGDATFRPNMIP
IPEECPLGPNPYGHTKVAIENLANDLNSDKKSWKPAILRYNPNIAHP
SLGLEDPLGTPNNLIPYMAOVAVNREKLYIFGDDYDSRDGTPIRDYIH
VVDLAKGHIAALQYLEAVNENGLCREWNLGSGKSTVEVYHAFCKASG
IDLPHYVTGRAGVNLNTAXPDRAKRELKWTQELQVEDSKDLWKWTE
NPFQYQLRGVEARSAEDMRVDARFTTIGAGTRFQATPANILGASIVDLKV
NGSVLGYENEGLYNDPSAIVIGATIGRYANRISKGKSLCNKDYOLT
NNGVANHSSIGSHRRKFLPGIIPNSKDVPTAEYNLIDNEKDETFPGD
LVTIOVTNVAOKSLEMYKGLTAGEATPINLTHSVFNLNKPYGDTI
EGTEIMVRSKKSVDVDMKMIPTGNITVDREIATFNSTKPTVLGPNKPFDC
CFVVDENAKPSQINTLNELTLIVKAFHPDSNITLLEVLSTPTVQFTGD
FLSAGYEARGQFAIEPGRYIDAINQENWKDCVTLKNGETVGSKIVYRFS

YDR345C, 2204 bp, CDS: 501-2204 (SEQ ID NO 123)

TCCTAGCTATATCTTCCAGCTTCCGCTGCTGCTGCCGCTCATCTCTCTGT
CAGCTAGTTTTCGGATTCGTCGGCTCATATAATACCCCAATAAACAC
CGAATATCTCTGCTCCGGATTCGGTTAACTCTCGCTCGCGGATTTATCA
TTGGATTTTCGGAGGTCTTATCTACTGACCGCCATTTATATGACTGTACA
ACGACCTTCTGGAGAAAGAAACAACTCAATAACGATGTGGGACATTTGGG
GCCACCTCAAAAATCTGGGACTATATCCCGAGAGAAATTTCTCCAGAAG
AGAAGAAAAGTCAAAGTTTTCCTGCTTGGGGGTTCATATAATAACAG
CGCTGCTTTTATCTTACACATAATTTTCAATTTTACTTAACTAGCTT
TTCATAAATAATAGAAATCACAAATAATTTACATCTGAGTTTAAACATC
ATGAATTTCACTCCAGATTTAATACTCCACAAAAGTCAAGTGAAGATTC
AAATGCTGACCTGCTTCCGATTAATGCTCTCAGGTAAATGAACATGCTGAAG
AAAAAGGTGTTCCAGATGATTTTCAAGAGCTGAGCGGACCAAGTGAAC
AACCCAAATACAGGTAAAGGTGCTATATGTCACCTGTGCTATCTGTGTGT

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TATGTTGTCCTTCGGTGGTTTTCGTTTGGGATACTTGTACCATTTT
CTGTTTTCGGTCCCAAACTGATTTCTTTGAGAAGATTCGGTATGAAGCAT
AAAGATGTAGTTATTTATTTCTTAAGGTTAGAAGTGGTTTAAATGCTCTC
CATTTTCAACATTTGTTGTCATTTGTTGGTATTTATTTTGGCTAAATTTGG
GTGATATTGACGGTGTAAATGGGTTGATTTGCTGTTGTTGTTATCTAC
ATCATCGGTATTTATTTTCAAAATTTGCATCATCAACAAATGCTACCAATA
TTTCATCTGGTAGAATTTATTTCCGGTTTGGGTTGTTGGTGGTATTTGCCGTTT
TATCTCTATGTTGATTTCTGAACTGCTCTCAAGGAAATGAGAGGTACT
TTAGTCTCTGTTTACCACATGATTAATCTTGGGTATTTTCTTGGGTTA
TTCTCATTTAGGTTTGTGTTTTCCTTGGGCTTTTATATGATCGGTGATAG
TTCTGTTTCCAGAAATCCCAAGCTTTATTTGGTGAAGCTGCTCAAAATTTGA
ACTTTGTTCCAGAAATCCCAAGCTTTATTTGGTGAAGCTGCTCAAAATTTGA
CGAAGTGAAGCATCTCTTCCAAAGTTTAAAGGTTTGCCTCCAGACCAATC
CAATCATTTCAACAGAGTTGGAAGTTATTTGAAGCTAGTGTTCGAAGAAGCT
AGAGCTGCTGGTTACGATCATTTGGGTTGATTTGTCATCTGTTAAGCCGGC
CATGTTTAAAGCTACTATGATGGGTATCATGATCCAAATCTCTACAACAAT
TGACTGGTGAATAACTATTTCTTACTATGTTACTACCGTTTCTTAAAGCT
TTGGTATGAGTGTCTTTCGAAACCTTCTATTTGTTTTCGTTTTCGCTCAA
CTTCTCTCTACTTTGTTTCTTGTACTACTGTCGATCTTTTGGACGTC
GTAACGTTTGTATATGTTGGTCCCATTTGCTGCTGCTGTTATGTTAGTT
TACGCTCTGTTTGGTGTACAGACTATGCGCAATGGTGAAGGTTAATGG
TTTCATCAAGGTTGCTGTTAACTGATGATGTTGCTTTCCTGCTGTTCTATA
TTTCTGTTTGTCTACCATTTGGGCTCCAAATTTGCTTATTTGTTTATTTCT
GAACTTTCCCATTTGAGAGTCAAGCTTAAAGGCTATGCTATTTGCTACAGC
TGTAAATGTTTGGGTTTCTTGAATTTGTTTCTTCTTCTTCACTTTTATTA
CTGCTCTATTAATCTTCTACTACGTTTCTTCTTCTTCTTCTTCTTCTTCTT
TTCCGCTACTTCTACTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
TTTGGAGAAGTCAATGATATGATGCTGCTGCTGCTGCTTCTTCTTCTTCTTCT
CTGCTTCTATGCTTCTTCAACATCTCAAGAGGCTTAACTACGATGCTGAT
GCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATAA

YDR345C, 567 aa (SEQ ID NO 124)

MNSTPDLISPKSSSENSADLPSSSSQVMNMPKGVODDPOAEADQVLT
NNTGKAVYTVTSICVMVAFGGFVGMNDGTISGFVAQTDFLRFRGMKH
KDSYVLSKVRTGLIVSIFENIGCAIGIIILAKLGMGRKMGILIVVVIIY
IIGIIIIQIASINKWYQYFIGRIISGLGVGGIATVSPMLISEVAPKEMRG
LIVCYQLMITLIGTFLGYCTNFKYNSVQWVRPLGLCFAWALFMIGGM
TFVPSPRYLVEAGQIDEARASLSKVNKVAADHPPIQOELEVEIASVEEA
RAAGSASWGBELFTCKPAMFKRMTMMGIMIQSLQLQTDNVPFYVYGTTFVNA
VGNDSFETSIIVFGVNVFFSTCSLYTVDFRGRNCLLYLGAIGMVCCYVV
YASVGTRLWPNGBEGSSKAGNMIIVFACFYIFCFATTTWAPIAVVVIS
ETFFPLRVKSKAMSIATAANMLWFLIGFTTPTTGAINFYGYVFMGCMV
FAYFYVFFVFPETKGLTLEEVNDYHVAEGLPKWSASWVPTSQRGANYDAD
ALMHDDQPPFYKMFGRKX

YKR097W, 2150 bp, CDS: 501-2150 (SEQ ID NO 263)

ATAGGAAAAACCGAGCTTCTTTCATCCGGCGGCTGCTGTTCTACATA
TCACTAAGCTCCGGTATTTTAAAGTTATACAGGGAAGATGCCCGCTA
GACTACAGTTTTAGGCTGCTTAACTATATGATAGCGGATGAAAGGC
CCAAACAGGATTTGAAAGCTTAGAGCTTCTGTTGGCAATGTTAGCTT
TGTGATTAAGTAAGGCTTGGCTGGGATAGCAACATTTGGGACAGATATA
GAAGACCAAAAAAAGGTATATAAGGGGAGAGAGTCTTTGTAAATG
TGTAACTTCTTCCATGTGTAATCAGTATTTCTTACTTCTTCTTAAATG
TACAGAAGTAAGACAGATAACCAAGAGCTTTCCAGAGATATACATATA
TCTTTTATTTTACAGCTTAAACATAATATATTTTGTTTTAACTCAAAAAATAA

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TCCGGAAAGATCAAGAGACTGCCAAATCGCACCTCTAAGAAGATGTGTTC
GCCATTACACACAGCATGTGTGAGAGACTCTCTAAGAGACATCAAAACC
GCTATCAACAAGCAGCAATTCGAATTCACGATAGAAAAGCAGGAATC
CTTTGACCGGATGTGTGTGGAATTTATGGCGAAGAAACGGAGTTGAACGCCA
AGAAAATCAAGGTGTCTGTGCAAGTTGTATGTAAACACAGATGGCGCAATG
GTAGATGTGATTACAAGACAGAACCCCTTGCAGCCACTCATCTAA

YL057C, 164 aa (SEQ ID NO 218)

MTKDKKAKGPKRSTIITKSGESLKFEDLDHDFETYLKGETEDQEPDHVH
CQLKYYPFVLHDHDDPEKIKETANSISKKFVRHLHQHVEKLLKDIKT
AINKPELKFHKKQESFDRIVMNVYGEETELNAKKFKVSEVVEVCKHDGAM
VDVYKTEPLQPLI

YDR544C, 929 bp, CDS: 501-929 (SEQ ID NO 135)

TAAAGTAGTCGGTAGCTACTTTCGTTTCAATTTCCATGGTGACACATAT
CTTAATATCTGCTAGTCGAGGAGAACAGAGATCTGTGTGCTCAG
CCGCTTCGTGGATATCTCTTGGATACCTTAAATATGAGACTACGCTTAG
CTCGCCTTAGCCCTACAATCTTCTCGCTCTCGAAAAGACCATAATA
GAAAGTTATAAATTACATTTCTCTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGAGCCCTTTTGGGTACTACATATGGCGGCTCAGACAGACA
AACTTCCGCCAAATAATGATTTACCCCGCGGAATAAGAAAACAGACCAAT
CACCACGAGCTACAAGTTACTTCTTGGTATGCAATGTCCTCACTATAAA
AAATCTCTGACCTAGATCTGGACTTAAATCTCGCTCACAATCGCCT
AAACAGGAATATTCCTATTTTCGTACAAGTTACTTCTAGATGCTAT
ATGTCTCTACGGCTTCTCTAACACCACTCAGCATGCAATACAGTGACAT
ATATATACACACACACACACACACACACACACACACACACACACAC
CCACACACACACACACACACACACACACACACACACACACACACAC
CCAGAGAAGCCCTAGCCTAAGACTAAGACAAGCCAAGCCTGACCAACC
TGCTCTCAAAATTACCTTCCATACCTTACCTCCCTCCTGTTACCTGTA
CTCATTAACATTAACACCCCAACCACTCCCTCCTGCTGCTGATACCC
ACCAACGACCGTCCACCACTACCGTTACCTCCCAATACCCATATCCAA
CTCCACTACCACTACCTACCATCTCCCATCTACTACTACCATACTAT
TGTTCTACCCACCACATTTGAACGGTAA

YDR544C, 142 aa (SEQ ID NO 136)

MSLRPCLTPSSMQSDIYIHTPHPHPHHHTHTPTPHPHHTPT
PERSLSLRQAKPDQPVQSITLHYPTSPVLTLSHTIPPQPPSISLCTT
TNRPSITVTLQLPISNSTTYPISHLULLILLPYPLPKR

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 255)

GGCTTTTTCAGTCCGCGGCTCGAGATCCAGGCACACAGGAATAGGCA
CGCTGTGATTCTAACATATGAAGGCTAGGCGGCTGACGTGGGTC
TAGTTCCACTTTTCTATCTTCTCTGCTCTTCTTCTGCTCCACAGG
CCGTTAATGGCTGAACAGATTTGTGACTTTGGACTTATGATAAGATG
TTTGTCGGGTGCGCAGGATCTATCGCGGCAATCAAGTCTAGTCTGT
TTGCATCATCAAGGCACTGCTCATTTGTGTAAATGTTCTAGCCTTTG
TCATCAATATATATAACTACAGCTCAGAGCTAGGTGCTGCTGGCAG
TGGTAAGTAGGGCTGCTTTTGTGCTATCGGCCAATACTGTTCGACGG
CCGCGCTGAGGCTTCTTCTGGCTTCAACCTTAGAGCTGATACCTTTGCT
TGGTCAAGGGCAAAAGCTTACTCTCGCTTTCAGTCTGCTTTTCCGTTTC
ATGCTGCTTTTCAAGGGTCTCTTTCTGCTCTCGGTGTGAACACACTGT
AGCTGCTATGCTTTACCGTACTCGGAAAGGCTAGCCCTCATGACTAGTT
GTACCAAGCCCTTCTTTCTTTCTTTCTTCTGACACTTTCGGGCTATT
CATGCCACTGGTACAAGCGGATAGGTGCTTTTTCCTCATTTTGGTTTT
GACGTGCGATGTTCTGCGGACCAATCGCATGGGTGGTGGATGTTG
TCTTTGCTAGTTGCAAGCTAGTCTTCTCTCTCTGCGCTTTCTGACGAA

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AAATGGCCTTACGTATCTTTTTCGGCGTCTGTCTGTCATCGCTGTTC
TATATAGTGTGTCATCATATCGCGCTTTTACTGTCATGCTGTCTTTTGA
AGAGAGTTTTCATTTGAAAGTAGTGAAGAAAAAAGAAAAAAGAAAA
AAAAAGAAAAAGCTTACATACGGAAGAGAAAAAAGAAAAAAGAAAT
TTAA

YKR040C, 167 aa (SEQ ID NO 256)

MTSFQVSAFALCNTLVACYAFTVLEKRSMTSCTNALSFLFLTLRRI
HRHWKYPGAPLLIFVLTLBWRFGPIAWVVVDFVASCNVVFFSPALSD
NWPYVSFFGVVVVIAVIIIVVTHIGAFACCLLKRSLKSEEEKKKKK
KKEKSLHTEREKKKKKX

YNL338W, 659 bp, CDS: 501-659 (SEQ ID NO 337)

TAAAGTAGTCGGTAGCTACTTTCGTTTCAATTTCCATGGTGACACATAT
CTTAATATCTGCTAGTCGAGGAGAACAGGATTTCTGTGCTGCTCAG
CCGCTTCGTGGATATCTCTTGGATACCTTAAATATGAGACTACGCTTAG
CTCGCCTTAGCCCTACAATCTTCTCGCTCTCGAAAAGACCATAATA
GAAAGTTATAAATTACATTTCTCTATTAGGTATACGACCTCGCGCTTCGA
AGTAGAGAGCCCTTTTGGCGTACCTACATATGGCGGCTCAGACAGACA
AACTTCCGCCAAATAATGATTTACCCCGCGGAATAAGAAAACAGACCAAT
CACCACGAGCTATCAAGTTACTTCTTGGTGAATGTCTCCACTATAAAA
AAATCTCTGAGCTAGTAGCTTGGACTTAAATCTCGCTCACAATCGCCT
AAACAGGAATAATTCCTATTTTCGTACAAGTTACTTCTAGATGCTAT
ATGTCTCTACGGCTTGTCTAACACCATCCAGCATGCAATACAGTGACAT
ATATATACCCACACCCACACACACACACACACACACACACACACAC
ACCCACACCCACACACACACACACACACACACACACACACACACAC
CTATTTCTAA

YNL338W, 52 aa (SEQ ID NO 338)

MSLRPCLTPSSMQSDIYIHTPHPHHTHTPTPHPHHTHTHTHNPNT
LP

YJR115W, 1010 bp, CDS: 501-1010 (SEQ ID NO 235)

GCAGTATCCCTTTCTGAATAAGCTTAAACCTTGAACACACAGGGGTG
CCGCGCTCTTAACCTTTCAGCCTCGCAGCGCGCTGAGTCGCGAATGTTG
CGGCGCTGCGCCCGCCGCAACACCGCGCCCGCTGCTCAGCTTAACC
GAAACACACAGGCTGCTCCATCTTCCATATACCTCGCTCTTCTTTCACA
ATGCCGCTCAAGAGCAACTGCAAAAGAGCCCGCTTCTAGTGGGTTT
TCCCACTTTGATATAACCCCGCCCGCCCGCCCGCCGCTCAACTGGTAA
TTTAACCAAAACACACGCGGTCTAATTTTAAAGCGAAAAACCTTAAAG
CGTTCTCGAAGAAATCTTCTCTAGTATGATGCTGAGCAAACTTATCTTT
TAGAGTGTGTGCTTACTGCTAGTATGATCAAAATTTACGTAGCGCC
CTTTCAACCCCTGCGAAGTAGTACATTAACAGCGGTAGTGAACGCTGC
ATGTTCAAAATACACGTACAATTTAATATACAAATAGTAAGGTGATGAA
CAGACACACACACACACACACACACACACACACATATATATATA
CAGAGATCAAGTTAGTGTGAGGAGCGACTACTGAGTTTGAAGTTCTTT
AAAGTTTAAAGTATTTTCTCCCTCTCCCACTCTGCGAACCCTCTCA
CCACCCCTTAGCAGATGTCTCCGTATGATGACCATACCTCAGCAATACT
TATACATAAGCAAGATAGTTCCAAGCTGCTCTCAGTGGCCCTTACTCGA
CACCACACAGAGAACTTGTACTACGAAAAATAGAGAAATCGAGCGGCTTACTCGA
GCTGGACAGGATCTCGACGAAATAGACGAAATCGAGCGGAGTAGTAC
TGTGTGACGCTGCGGATGTTCTTCTACTGACAGAGCTCATTTCCGCTTCC
CCAGCATCCAGCAGCTCTTCTCTCTCTCACTAATAACATCCGGCCCATAG
CATATATGTGA

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ATTGAAAGCTGTAGTAATATACAAAGCCCTTTTCCAAACATTCGGTTATGCTGGGACGCAATCTCAGAAA
CTCGCAAAACAATAGATATACTAACATGATTTCTTATATAAATCTTAATTTTGAATTTATTTCTTATATATAC
AGACAGGTGTACAGATCTCGTACTCGTATACATGTTCCAGGTGTAAGTTCAGAAAGCATGTCGCGCTCCAT
CTTTCTACTTACTTGAAGCTTACAAAGTGTGGTGCACATGTCGACATCAAGCCCAATGGTCTCATCCAA
AAGGTATGTCCACACAGATTTTACCAAGGTGAAGACGGTGTGTTCTACAAAGCTTACTTAAGTCTTCTGTT
GGTGTATCATACACAGATGTCGGTGAACAGTATCTAGAAAAGAGTAAATTAAGAGTTGAACAC
ATCAAGCACTCAAGGTGTAGCAAGAAATTTTGGAAAGAGTTAAGGCCAATGCTGCTAAGCGTGTGAA
GCTAAGGCTCAAGGTGTGCTGTTCTCAATTTGAAGAGACAAACAGCTCAACAGAGATCCCGTATCGTT
TCTACTGAAGGTAAAGTCTCTCAAACTTTGGCCCCAGTTCCTACAGAAACCTTTCTATCTAA

YBR191W, 160 aa (SEQ ID NO 62)

MGKSHGYSRSTRYMFQRPRKHGAHLSYLYLVKVKVDIVDIKANGSTQKGMHPKFYQGTGVVVNVTK
SSVGVIINKMGNRYLLEKRLNLRVEHIKHSKQCHEFLERVKANAAKRAEAKQAQVAVQLKRPQAPRES
RIVSTEGNVPQTLAPVPYETFI

YCL035C, 833 bp, CDS: 501-833 (SEQ ID NO 65)

CCGAAGAAACCCCATGTTCTTGTGTCCTGCTCCAATGCTTATATCACTCTCAACACTGTCACAAT
CGTGTGTCTCATCTTGAAGAAGATACACATTTGATTAACAACATATAAAGTTTAACTATTACCT
TGATCACTTTACACGTCGAAGTCAAAACAGTTTCATAGTTATCACTTGAAGTATGGCTCCATCATCTTA
TAAACATGAACCTTCATGCACAAAGTGAAGTGTCTACAGATAACGAGCAGCGCAAGGGTGTCCAGAT
TGCAGATGTTGTTTCTTATCTACTCTCTTACTACCCCTTGTGCGCTCTGATTCACGTGATGT
GGGAATTTTGTGGAAGGATTAATATAATAATAAATAAAGTTTATATAATAATAAAGGAGCT
TTAGCATATAATAAAGAACTCTGTGAGTACTTATACGAGCATTCGCATATAATATACAAATAGACAAAA
CCTCAGAAAGGAAAAAATGTTATCTCAAGAACTATCAAGCAGTCGAAGACCTTATTTGCAGAAAACG
AGATCTGTGCGCATCCAAAGCTACTGCTCATCTGCAATGCAAGCCCTAAACAGCGCTTTTGTGAAGAAT
TAAAGTTCCTCAGGTCCAAAGTCTGGTTTGGCAATTTGAATGATCATGAAGGAAGGGCAGACATTCAGG
CTGGTGTATCAGATTAATGCAAGAAACCGTCCAAACATCTATATTAATGTTAAACATATCTGGAG
GCAACGAGCACTTGCAAGAAATTGAGGGAGACTGGTGAATTTGGAGGAATTTGTAGAACCTATTCTTGCAA
ATTAA

YCL035C, 110 aa (SEQ ID NO 66)

MVSEETIKHVXDLIAENEILFVASKTVCPCYCHAALNTLFEKLKVPRSKVLVLQLNDMKEGADIQAALYEI
NGQRTVNIYINGKHIGNDNDIQELRETNGBELELLEPILAN

YDL004W, 983 bp, CDS: 501-983 (SEQ ID NO 81)

ATAAACATAAGATATAATAGTTTTTAAATGGTCAAGTATGCCATGCAACAACCTAAAAGGTACCAATTC
ATTAAATATTATTAATATTACTTTTACTATTACAGAAAGACAAAGTGTGAAATGCCTAGGAGATTGAT
GATTCACAAGCTCTGGCTTGGCAATAAATACTTATACACAACCTTCAAAATATATAGAAAAGAAAGAA
GACTATAAGCTTAAATAATGTAGACAACCTTCATTTAAATATTAATCTTAGGACTTGGTAATAATAGCTAAT
TTGTATATTATTCACCTCGCTCACCGCTGTATCACTTTTAACGAAATAGATGCCAGCCCAATCAAA
CGCATATTAGGAGTGTGTAGGAAGGGCGCTCCCATCATTTGTAAGTTCATGTTTAAATTTAGATGGAG
GATTAACAATAAAGGTATGTCACACACTGTCAAAGAGCCCTCAATCAATTTGTGAAGTATNACTGTGA
CGCGTGAGGATAGGAAAAATGTTACGTCAATATTGGAAAGAGTGCATCAAGATCAATGCAATTTCTGTG
CTAAGCGTTCATATGCAGAAGCTGCTGCCCATCATCAGGTTTGAAGTTACAAATTTGCTCTACCAACG
AAACTTTATATAGTGTCCCGAAGTTACTCAAGTACCTGCCCTGTGAAGTCAGGACATGTTGGTGTAT
TGGCAACCATGTTCCCATCGGTGAACAAATACTACCAAGGTGTGGTGAAGTTAGGAAGGCTCTAACT
CTAAAAAATCTTTATATCAGGTGGATTTGCAACAGTGTCAACCACTCGGAGTTATGTGTAACTGCA
TTGAAGCTTTTCCATTTGGAATCTTTTTCACAGAAATAATAAAAAATTTTGTGGCAGGAAGCTTAAGAAG
ACGTGTAGTTCATCTGATGCCAGGGAAGCCGCAAGCTGCAATTCAGTAGAAGTTTTAGAAAAACCTCA
AATCCGTTATTGAATAG

YDL004W, 160 aa (SEQ ID NO 82)

MLRSIIIGKSASRSLNFVARSVAEAAAASGLKLQFALPHETLYSGSEVTVNLPAKSGRIGVLANHVP
TVESQLLPGVIEVMEGNSKKFTISGGFATVQPSQLCVTAIEAPPLESFQENIKNLLAEAKNVSSSD
AREAAAAIQEVLLENLQSVLK

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YDL075W, 1263 bp, exon1: 501-557, intron1: 558-978, exon2: 979-1263
(SEQ ID NO 85)
ACTATATTTGTGTTTTCCCGAACCTCTCCCTCTCTGGGCCCTTTTTCCTCATATATCAAAATATTTTTCATAC
CTTTTACCTCCGTACACCAATCTTATTTTACCCCATACCTTTGTATTTCTGCAAAATTGAGAAATGATTT
GTGGTGTGTTTTTTTGGACATCTGCCCTCTGTGACAGTGTGTTTGAACGCTAGCGCAGCATGTTTGGCAA
CGGAAGGAAGTGGGAGAGCCAGAAAGCCCTTCTCTCGCATGGTGTGATCATCTTCTGCGAGCGGAGGAT
GGGAAGCTCCGTTCCAGGTTTGGCGCTTTCTTTCTGGCATTTTGTCTCCCAATTCGCGCAGCAGAC
ATAGCTTGACATTTACTCATGCTGCGCATTTAGCGGCTTGAATCTCATAGCTTGAAGATAGTATTTGAATTT
ATATTGAAGATTTTATAAATACTGTGATAAATTTCAATCAAGTTTAAAGAAAGAAATTAATTAAGCAACAGA
ACTCAATCAAAAGGAAATATGCGCGGTTTGAAGAAGAGGTTGTCACTCTGCTGAATACACCATTAACTTGCACA
AAAGAGTATGTGAAGAATAAATAATAATAATGCCCCAAGGCTGTGCTCATCTGAATGGTTTAAATAGAAAG
ATTTCTATAGTCAAGGAATACATAATACAAGAAATTTGTACCACAGAACCTATCAACAAGATCATTTGAT
CAAGATATATTTTATAAATACCGAATTTGAAGACCATTAATATATATATATATATATATATATATATATAT
ACACTTCGGCTGGACTTAAAGAGCGATGAAGACAGAAATAGTTATCTTAAATAGTGGAACTCTCAGATTTT
TAACTCGCAATATATCCATATCCCAAGTTTGACTAAATATGAAATCAGAAACAAATTTGGGTCTCCAATATA
CAAAACCATTCATCAAGATTACATATATATAAATGAACAACTCGTTACTAACAAAAAATTTTACCATT
TATTTTAAATAGTTGACGGTGTCTCTTCAAGAAGAGAGCTTCCAAGAGCTGTCAAGGAAATTTAAGAAG
TTCCGCAAGTTACACATGGTACTGATGATGTCCTGCTAGCTCAGAAATTTGAACCAAGCTATCTGGAAG
AGAGTGTCAAGGGGTGTTCAATACAGATTAAGATTGAGAAATTTCCAGAAAGAGAAACGAAGAAAGAC
GCCAAGAACCCATGTTCTCTCTACGTTGAACCTGCTTAGTGTCTGCTGCCAAGGGTCTACAAAATCTGTT
GTTGTCGAAGAAGATGCTTAA

YDL075W, 113 aa (SEQ ID NO 86)

MAGLKDVVTREYTNLHRLHGVSFKKRAPRAVKEIKKFAKLHMGTDVRLAPELNQAIAWKRGVKGVEY
RLRLIRSKRNEEEDAKNPLFSYVEPVLVA SAKLQTVVVEEDA

YDR064W, 1495 bp, exon1: 501-521, intron1: 522-1060, exon2: 1061-1495
(SEQ ID NO 89)

TGACGGTGTGTACAGGAATGGAAGATGCTTTATGCCGGCGCATATAGAAATGATCAGAGAGAGTGCGG
GTACTTTTAAATTCATAGAGTTTCTTCAGGTTTGGAGGTGACTCAGACGTTTGAAGAAATTTGAGGAGC
AATTAGAAATTTGTAGTATGATCTATCTTAAACACTAACTCTCTCTCTATATATCATGTAGTGTACTTT
AAACATTTTTTTTATCTTCATGCAATATATAGCCCTTTTACCACCATTAACCATTAAGTAGACCCCAA
ACATTTTTTAAAAAATTTTACGTTATAATTTTCTTGTCTGTTTCTGAGCGCGCAAGAGTAGCGGT
GAAATTTTGATACGAATGAGATTTCCACTCTCTGTACAGATGGAATTTTATGTTGGCCGACATATATCAC
AGTGTGATGAATTTAAACAATTTCTCTCTCATTAATATTTTCTTAAACGGTTTAAACCATTAATCAATC
AACACAATCAGTCAAAATGGTGTGTATGCACAGTGCCTGATGTTTATTAACACCATAGGAGATATTA
ATGCAAAAGTTGCAATGTAATGATTTGCTGCTAAATCAGATGACACTTAATGTGGAATTTCAAAAAGTGGATT
CTAATATAATTTGCTCTGTGCGATCACAATTTCTATTAACAAGTTCCGGTGTGTACACAGGTATATGTTTA
TACTGGAGAGTATGTTTCTACTGCTGTACATTAAGCTGGGTGATTTCCCAATTTCTTTTACAAAATATGTTGC
ATTAGTTTAAACAGGTTATACTATCTGCCCTTTTCTCAGTATAATTTACGCCGGAAAAATTTACTGATGGCTA
GCCGCTTTTATGAATTTAACTTTTCAAAAGCTCATAAACATAAACAGCTTAACCTATCGGAGAGAACCAAG
ATTGAAGAAATCACCCGGAATAGTTATCTTAAATGGAATTTGTATGCTGTGAACGAGGAATATGTCATG
ATACACTTTTCTCAAGCCATATGAATCTTCATGTACTTAACATTCGATTAATTAATTTTGGAAATATCCAA
TTCCACTTAATATTACTTTAAACAGGTTAAAGTATTTCTTCTTCTGCTATTTCCATCTCTAGAAATGC
TCCAGCTTGTGTTGAAGTTCTCTGAACTGTCAATTTGAACAAATTTGCAAGTACGCGAGAAAGGTTT
GACTCCATCTCAATTTGTTGTTGTGTAGAGATGCTCAGGCTGTTTACCAGCTGCTGTGTATCATCTG
TAAACAGATCTAAGAAATCTTGAAGTCCAAATGTTGCTGCTCAAGAAATCCCAAGAGATTTGTACTACTT
GATTAGAAGGCTGCTCTGTAGAAAGCACTTGGAAAGAAACAGAAAGGACAAAGACCGCTAAGTTTACG
ATTTGATTTTGAATCCGAATTCACAGATTTGGCAGATACTACAGAACTGTTCTCTCTCTCTTACCCACC
AAACTGGAAGTACGAATCCGCCACTGCGCTCCGCTTGGTCAACTAG

YDR064W, 151 aa (SEQ ID NO 90)

MGMRHAGKGGISLPAIFYSRAPAWFKLSSESVEIQIVKARKGLTFSQIGVLLRDAHGVQARVITGN
KIMRILKSNGLAPEIPEDLYYLIIKAVSVRKHLERNKDKDAKPRLLILIESRIHLRARYYRTTAVVLPNN
WKYESATASALVN

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YDR099W, 1322 bp, CDS: 501-1322 (SEQ ID NO 93)

YD9039W, 1342 bp, CDS: 302-1342 bp
 TTGGTATGACGCAATCCGTAATTCAGCGGGGATTCATATGACAGAGATTAATATACAGGAATACCT
 ATTGAATATGCTCCCTTTTGTGTTTAGGAAGAACGGAGCAATGGTCGCTGTCGCAAAATGATTAAGTAGT
 GTGTACCCCGGATACGACAAATGACACACAGCAAAATGAGAAAAATGTCGGTCCAAAGGGCAATGT
 TATTTAATAGTCCCTCAGAGTCTTTTGTGTTTTCAAATATTCATATCAATCAAGGTACGAACCTTTTGA
 GCTATCTTAAATCATTGCTTTTATTTTTCAAATTTTACATTTATTTTTCAAAAAAAATTCGCT
 CTCACGATGCAATTCGTTCTTTTATTCAAATTTTCAATTTATTTTACGAGGAAAAAGAACAGAGAAAATCTGGA
 CTCCCGGTATTAATCATTAATTTTTCGATTCATTTAAGGGGAAAAAGAACACAGAGAAAATCTGGA
 CAGAAGTTAATATCTGCAATTTTCAAAACGAAAGAAATTTCTTTTACCTAGTAATTAATCAATCAAAAAGTAC
 CCGTATCAACAACAAAATGTGTCAAACCTGCAAACTGTAAAGATTTCTTTTACCTAGTAATTAATCAAGAC
 CGGAACGATATGAGAAATGTGTCAAACCTGCAAGCCGTTGCTTATCAAGGTCAAGATTAATCTGTGCG
 AAGAACGATATTAATGTGTGTGTTTCAAGAACTGATCTGGTGTCTGCGCGGTCTTCAAGGAATAG
 TTTCTTCGATCGAACAAGAAAGAAATCAAGAGAAATCTGAACTTCAAGTGAATTAATTCGCTTCTT
 ACCGTTCTAAATTTGAACATGCAATGCAAAAATCTCTGACGACATTTATCTGTGTTATTCCTGTTT
 TATATCCCTTCTGTGTACTACTGTGTGATGTCCTAAATTTTATTAAGTATGAAGGTATCATCAACCGCTT
 ATTTAGCTCAATTTTTCAGGAGGATGTCGACAGAAAGGCAACCACTCCTCTTTGGAAGCTTATAAA
 CCGCTTCCGAAATTCGCCACAATGAAATTTGCTCCATCTCAACCAATTCGTTTAGTCTAGCTTTGATTT
 TCTCCGCTTCTTAATTCGAAATTCAAATCTCCTGTGAATGAGCTTGCACCTGAGTGCACAAACGCTTGT
 ATGATCTAATGTGCTAGTATGATATCTTATCTGAATATCATCAAGATPAGCACTTGTATCATGCAAT
 TATTTAAAGGCAACCTGATACCTTAAGACCTCTGATTAATTTGATATGTGCTAAGAGATCAACAACAC
 AACCAAGCAACGACCAACGCAACAGCAACAGCAACGCAACCAAGCTTCAGTGAACAAATCAAGGTGAC
 CAACCAATATA

YDR099W, 273 aa (SEQ ID NO 94)

L0T1LSE8EYVDSTLMQJLRNULWMTSDISESGEDPQQ000000000000QAPEAQTOGEPTK

YDR134C, 701 bp, CDS: 501-701 (SEQ ID NO 97)

YDKH394L, 101 bp, 500-500 bp, 1000-1000 bp, 2000-2000 bp, 3000-3000 bp, 4000-4000 bp, 5000-5000 bp, 6000-6000 bp, 7000-7000 bp, 8000-8000 bp, 9000-9000 bp, 10000-10000 bp, 11000-11000 bp, 12000-12000 bp, 13000-13000 bp, 14000-14000 bp, 15000-15000 bp, 16000-16000 bp, 17000-17000 bp, 18000-18000 bp, 19000-19000 bp, 20000-20000 bp, 21000-21000 bp, 22000-22000 bp, 23000-23000 bp, 24000-24000 bp, 25000-25000 bp, 26000-26000 bp, 27000-27000 bp, 28000-28000 bp, 29000-29000 bp, 30000-30000 bp, 31000-31000 bp, 32000-32000 bp, 33000-33000 bp, 34000-34000 bp, 35000-35000 bp, 36000-36000 bp, 37000-37000 bp, 38000-38000 bp, 39000-39000 bp, 40000-40000 bp, 41000-41000 bp, 42000-42000 bp, 43000-43000 bp, 44000-44000 bp, 45000-45000 bp, 46000-46000 bp, 47000-47000 bp, 48000-48000 bp, 49000-49000 bp, 50000-50000 bp, 51000-51000 bp, 52000-52000 bp, 53000-53000 bp, 54000-54000 bp, 55000-55000 bp, 56000-56000 bp, 57000-57000 bp, 58000-58000 bp, 59000-59000 bp, 60000-60000 bp, 61000-61000 bp, 62000-62000 bp, 63000-63000 bp, 64000-64000 bp, 65000-65000 bp, 66000-66000 bp, 67000-67000 bp, 68000-68000 bp, 69000-69000 bp, 70000-70000 bp, 71000-71000 bp, 72000-72000 bp, 73000-73000 bp, 74000-74000 bp, 75000-75000 bp, 76000-76000 bp, 77000-77000 bp, 78000-78000 bp, 79000-79000 bp, 80000-80000 bp, 81000-81000 bp, 82000-82000 bp, 83000-83000 bp, 84000-84000 bp, 85000-85000 bp, 86000-86000 bp, 87000-87000 bp, 88000-88000 bp, 89000-89000 bp, 90000-90000 bp, 91000-91000 bp, 92000-92000 bp, 93000-93000 bp, 94000-94000 bp, 95000-95000 bp, 96000-96000 bp, 97000-97000 bp, 98000-98000 bp, 99000-99000 bp, 100000-100000 bp, 101000-101000 bp, 102000-102000 bp, 103000-103000 bp, 104000-104000 bp, 105000-105000 bp, 106000-106000 bp, 107000-107000 bp, 108000-108000 bp, 109000-109000 bp, 110000-110000 bp, 111000-111000 bp, 112000-112000 bp, 113000-113000 bp, 114000-114000 bp, 115000-115000 bp, 116000-116000 bp, 117000-117000 bp, 118000-118000 bp, 119000-119000 bp, 120000-120000 bp, 121000-121000 bp, 122000-122000 bp, 123000-123000 bp, 124000-124000 bp, 125000-125000 bp, 126000-126000 bp, 127000-127000 bp, 128000-128000 bp, 129000-129000 bp, 130000-130000 bp, 131000-131000 bp, 132000-132000 bp, 133000-133000 bp, 134000-134000 bp, 135000-135000 bp, 136000-136000 bp, 137000-137000 bp, 138000-138000 bp, 139000-139000 bp, 140000-140000 bp, 141000-141000 bp, 142000-142000 bp, 143000-143000 bp, 144000-144000 bp, 145000-145000 bp, 146000-146000 bp, 147000-147000 bp, 148000-148000 bp, 149000-149000 bp, 150000-150000 bp, 151000-151000 bp, 152000-152000 bp, 153000-153000 bp, 154000-154000 bp, 155000-155000 bp, 156000-156000 bp, 157000-157000 bp, 158000-158000 bp, 159000-159000 bp, 160000-160000 bp, 161000-161000 bp, 162000-162000 bp, 163000-163000 bp, 164000-164000 bp, 165000-165000 bp, 166000-166000 bp, 167000-167000 bp, 168000-168000 bp, 169000-169000 bp, 170000-170000 bp, 171000-171000 bp, 172000-172000 bp, 173000-173000 bp, 174000-174000 bp, 175000-175000 bp, 176000-176000 bp, 177000-177000 bp, 178000-178000 bp, 179000-179000 bp, 180000-180000 bp, 181000-181000 bp, 182000-182000 bp, 183000-183000 bp, 184000-184000 bp, 185000-185000 bp, 186000-186000 bp, 187000-187000 bp, 188000-188000 bp, 189000-189000 bp, 190000-190000 bp, 191000-191000 bp, 192000-192000 bp, 193000-193000 bp, 194000-194000 bp, 195000-195000 bp, 196000-196000 bp, 197000-197000 bp, 198000-198000 bp, 199000-199000 bp, 200000-200000 bp, 201000-201000 bp, 202000-202000 bp, 203000-203000 bp, 204000-204000 bp, 205000-205000 bp, 206000-206000 bp, 207000-207000 bp, 208000-208000 bp, 209000-209000 bp, 210000-210000 bp, 211000-211000 bp, 212000-212000 bp, 213000-213000 bp, 214000-214000 bp, 215000-215000 bp, 216000-216000 bp, 217000-217000 bp, 218000-218000 bp, 219000-219000 bp, 220000-220000 bp, 221000-221000 bp, 222000-222000 bp, 223000-223000 bp, 224000-224000 bp, 225000-225000 bp, 226000-226000 bp, 227000-227000 bp, 228000-228000 bp, 229000-229000 bp, 230000-230000 bp, 231000-231000 bp, 232000-232000 bp, 233000-233000 bp, 234000-234000 bp, 235000-235000 bp, 236000-236000 bp, 237000-237000 bp, 238000-238000 bp, 239000-239000 bp, 240000-240000 bp, 241000-241000 bp, 242000-242000 bp, 243000-243000 bp, 244000-244000 bp, 245000-245000 bp, 246000-246000 bp, 247000-247000 bp, 248000-248000 bp, 249000-249000 bp, 250000-250000 bp, 251000-251000 bp, 252000-252000 bp, 253000-253000 bp, 254000-254000 bp, 255000-255000 bp, 256000-256000 bp, 257000-257000 bp, 258000-258000 bp, 259000-259000 bp, 260000-260000 bp, 261000-261000 bp, 262000-262000 bp, 263000-263000 bp, 264000-264000 bp, 265000-265000 bp, 266000-266000 bp, 267000-267000 bp, 268000-268000

YDR134C, 66 aa (SEQ ID NO 98)

MOFSTVASIAIAVASA SNTTATVTEESTIMLVILISCEDHVCEI VSFADVSIAAVANV--

YDR171W, 1628bp, CDS: 501-1628 (SEQ ID NO 103)

IDRLIWM,LCZUP,GBS,CAA
 CTGGGGTGGGTGCAACAGTGTGCGAAGGAAAAAGTGAACATTTTAAAGAAACAAATTTAAATATGCAAG
 ATGGAAATGGTAATGCTTGGCTCTCGAAGAGGTATGACATTAACAGAACTGTGTTTCCCGAGATAAATTGG
 ATACTTCATATACGCTTTCCCTATGACCGCTCGAGACAGTAAATAGTGCTGTTCGCGAGATATTGG
 CGGAGGCCAACAACGTGGCTAGGCGGCAAGCGCTGTGAAAGTTTGTGAAAGTTCCCGAAT
 TGAGAACTGCTCAGGGGCGGAATACAGGGGCGGCTTTGGCGGCGAGGGGGAGGCGCTCTGTGTAAGTTAGTT
 ATATAGACTTGTGCTGTCACTGTTTTTTTGTGATCCCGCAGAGAACTATCTTTATCTCATATACATGCTTC
 AAGAACTATATTTATACATTAACATAGGCAACGTTTACGGCAATTCCTCATATCCCAACAAATATAGAT
 CATACCAGGCCGAAGCATGAGTTTTTATCAACAGATCCCTATCTTTATGACGTTTTTGAACGATTAAT
 CCAACCAAACTGGCGCAGAGGGCAGCAAGATATCTGCGCAACACAAAGCGCACAGAAATACATCATC
 CCCATTATGCAACAAGTGCAGCTTGGCGGGCANTCATCTGTCATCATCCATTTGTAATAGCAATACAAATG

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GTGTTTCCCTAATACCTATTATCTAACCACTTCCCTGAGCAAAAGCCCTATTACTATAGTCCATGATACATGACGCTTATG
ATGACGAGGATGAGTGAACAAAGAGCAACCAAGGAAGATATGCTGGGTGACACGCGCATCTACAGACAGAG
AAGATGCTGGCGAGGACAGCAACCACTGGAAGAGATATCATCTATTATCACTTGTAATATCTCCAGGAATAT
ATAGAGCAACCAACAGGCAACAAGTTTAAAGACTTATTAAACCGCTTATATAGTGTTTCCACCATATG
AAGGACCTGAAACCAAAATTTGAGCAAAATCCGAACAGAGGCGCAAAAAGGAGAAAGAAAGATATGAG
AGGATTAAGCTCTAGACACCCCAAGAGAAAGCTGGGGGAAACCAAAAGAAACCTTTGATACATCTAGCTG
AGGATATGCTGACACCATATGAGCCAAATCTTTCATCTGTTCCTCACTACATCAAGCGCTTCCCAA
AAGGATATGCTGACACCATATGAGCCAAATCTTTCATCTGTTCCTCACTACATCAAGCGCTTCCCAA
TACTGACACCCCTTAAAGATATCCAGTCTTCTTCCGTTTCCAGGTGCTCAATCTTACAGGGGCTTCCACA
TCTAGATATCCGAGGACACTTACAGTATGTTTCTTCCGTTTCCAGGTGCTCAATCTTACAGGGGCTTCCACA
TTGATATCCACATCTTCTTATGATAGTCTTACAGGTATGATGGAAGATCGACAGAGTGGCATTTGATG
AAAAATTTCTTGAAGATCAAGGAACCTTAAATATGCTGCGCTTTTGAGAAACCGTTAAATTTCCCGTGTCC
CAGCATTTAGGACAGCAAGAAATTAAGCTTATCTTACACAGCGCTTATCTACAAATTTAAGGTGCTAAAT
TTGTCTCATATCAAAAGAAAGCGCAAGCCAAAGAGAGAGATCCGCTATGAGGAATATCCGACGAGAAATTA
TCGAGTTTGAAGAAATATCCCAACCTTACGCTGAGAAATTTGA

YDR171W, 375 aa (SEQ ID NO 104)

[illegible]

YDR399W, 1166 bp, CDS: 501-1166 (SEQ ID NO 129)

TNGAATGCGCTATTGGAACAGGGCATGTCATTCTTATTCGAGCAGGAACACAAGCAT
 TCGTATTACCTTTTGTGACGTGATGCTGCGATCGTTAACAAGTAAAGCCATCTGGAACATCAAGCAAGGAC
 TCCACTTTTAACGCACAAACCATGATGTGTTAATCAAGAAAGACAGCATATATTTCCCTTCGAGTAC
 TTATTTTATTTTCTTCTGTAATAATTAATTAAGATTATTTCAATTAATTAATTTCCGGTATTTGAC
 TTCTTTCAATTTTTTTCTGTAATATTTGCGGTATTCAGGAAGAAAGGAAAAAATTTTTTCCCTTC
 CACTGTCTCCAAATCGGGTAGCGATGAGCTGCTATAGAAATTTTCTATTTTAAACATGTTTAAATAGGCCA
 ATTTCGGTAAAGATTGTGTTCCCTTCGAGAGTTGTGTTGCGGTATCTTTTATTTATTTAGTCTCATCT
 AGCTGGAAGATTAAGATGATGTCCTTTGATTTCTTTATTTAATTAACGGTGTGTGCTCATATA
 TCCATTACGTTCCATATATGTCGGCAAGACGATAGGAACATCATCTGTACACACATCATCACTAT
 TGCACAGTATCCCGTGAAGAAATTAAGAAATTTCAAGCGGACCTTAATCATTTGCCATGTGTGTGGCTT
 TCAATTCCTGTAGAGATCCTACGTAACCTTCTTAAGGAAGCCCGGCGTCAACATCATCAAAATTTTTCCTA
 TTAATTTTGTCTTGTGAGGAATTTGAAACAGTATAGGCTCAGAAAGTGAAGATGTGTATAGGTTA
 GCGAACACATAGATATGATTAAGACAAATGTAATTTAGTATAGTGTGCGAAGAACTTTTATTCGTTG
 ACGCAAGTCGATGACACCCGTCACCACTTCTATACGTTTGAAGTAATTGGAAATGGAGATGACGCTGAAC
 AGCCAAAGCTTAAGGATGATGATACAGCAAAAGTCTCCAGATGAAACAAATCTTCGGAGATTTTTC
 TACAGCTTAAGCAAAAACCAAGAAAGAAATTTGCTGCGGAATGTGAATATACAAAGAACTGTTATTC
 TTACAGCTTAAGCTTCCAGAAAGTGTATCATATTCATGGAAATCTAATCAATTTGTTTTCATTA
 CTAGAAATGGCTATTGGAACAGGGCATGACATTTTATTTCCGAGCAGGAACACAAGCATG

YDR399W, 221 aa (SEQ ID NO 130)

LMDZDRIY
 MSANDZKQYI
 EDNANSVSEVE
 IDPEKSEBMTK
 QGANDIFIRPEQ
 HENKQ

YDR418W, 998 bp, CDS: 501-998 (SEQ ID NO 131)

TGCACCTGTGAGTATTTGGTGTTTGCTATTTTGCTTCANMCAATACAGATATTTTGTTAGAGAAAGTGGAA
 ATAAACAATATCAATAAACAAAGTATCTTCATAGACCATAAAGCAATACCAGATATTCCTTTAGATAGACC
 AATGCTAATGTAACAGAGAAATCGTTTATGCGATCTTATACATATAGATATGCTATCTTGGCTTTGTGG
 TTTCAGACAGCTGTGCAGTCCCTCTTAGCCGCTTTTTCCTTCGAAAGGTTTCCGCTAAGACCCCTGTATG
 GCTGTAGGCCAGAGAAATGTTAAATGCTCTCTTCACAGAAATATGTTTGGCACATACACAGACAGCATGCG
 TGCAGACAGCTTCCGGAATCTTCTCAATCTGTATCTCTTTGGCGGTACCTTACATAGTATGAAATAT
 GGATATAAACAGTATCTTAATTTTACTTACTCTCCGTTAAAGCAACCCCAAGTGCCTAATAGAAAGG

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RHFHYDYDTATTTTTRTTPAIVTEPTEGKLTTEYGVSTIFDIHQRLTVQEMEPAPAGOLPRSIDV
ILDDLDVKTCKPGBRVNVGVTKSIGAGGMOGNSNWLIGFKTLILGNTVPLHARSTGVARQMLTDF
DIRINKLTKKKDIFDILSQSLAPSTVGHDKKALLMLMGVEKMLENGSHLRGDIINILMGDPSHA
KSQLRVLANTASLAIAITRGSSVGLTHAIVTDBRETERLREAGMVLADIRGVICIDEDPKMTDVR
VAIHEWEOQVTVLAKAGHTTLNACSVIAANPVFGQYDVNRDPQNTALPSSLRFDLFVYTD
INERDSDISSEHVLATHRLPGVLEGEVPERLNLAVGEDADINPEEHSNGAGVENGEDEHDV
FEKRNPLQAGAKLKNKNGVNTLPLKVLTPPLKRYVYAKERVLPOLTEALINIVKRYETDLRND
NTKPSITARLETILRLATAHAKVBLSKVNVDAKVAANLLFALGEDIGMDIEESEEELSK
RSPKSPKRRORVRQPSNSGSPKSTPRRSTSVSNATSSARILRFPQDBQMGAGDDNDIMSPAP
DEBELQRLQGLVSPRBEHLHAPBEGSGPLFEVGTPLRVNSAGQDDQDQSVISFDNVEGT
ISTGRSLISGILARMOTEIFEESYPVASLPERINEELPEEKFSQOETLAGLKIMSDNNINLVAD
KVWV

YGR146C 1136bp CDS: 501..1136 public: 1..1136 (SEQ ID NO 699)

CTTTCAGTGGGCATCTTTTTCCTTTCACATAGAGCCGCCCTTTTCCCAATTGGCAGCTTGTGTA
CGATCTTAGCTAGACCTGGAGACCTGGAACGTCGATTCCTATATTAAGGAATACCGATCTTCTT
CCGTTTCAACACCCCAATGTGGAATTTTATTTCTTTCGATTCGGAAATTTAGATPACATTCACATCC
ATACTGGACACATATATATATATATATATATATATATATATATATATATATATATATATATAT
TGAATCTGTATAAGAACTTAGAACTATAGTGTCTCCCAAGAACTTAAATTTGAACCTTGAGCAAT
TATAAAGAGATAGCAAAAGAAAGAAATAGAAACAATACCTCGCTACGATCTCTCTTTTCTCTT
ATATAAAGAGCTCGAGATATATATATATATATATATATATATATATATATATATATATATATAT
TGCATATCATATATATATATATATATATATATATATATATATATATATATATATATATATATAT
CATCTCCACAGAAAGCAACATTAATATACAGAAAGATCCAAAGGCAATGAAACCAAGCAAGTTTAC
AATCAATAGATTAATATATATATATATATATATATATATATATATATATATATATATATATAT
TATCCCATCTTGCTATAAATAATCAAAAATCTTCTCATTCGATTAATCTCATCCACGCTTTCATCTTA
AAATTTTATCGATCAACACCTTCTCAGCGACTACCTCATCTTCTCATCTTCCGATCTTTCACATA
TCCCTTTTACAGATTTGGAAGAGCTAGACCTTATATATATATATATATATATATATATATATATAT
TAGCTATCTTGAAGAGAGCTATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
ACTTAGCCGACTCTCTTAGCTAGCTGATCTGATTCATATGATTCATCAAGGCAATTTGGTTACGAAA
ACAATGCGCACAGCAACAGATCTAATATATATATATATATATATATATATATATATATATATAT
ACAACCTATGGTTAGCTATCTCCCACTTA

YGR146C 211aa public: 1..211 (SEQ ID NO 700)

MTATFADYCTVCDRLIPTSPQKININTRKIQIDNETKSLQSNKLYCSEDKLXDSNPINELKLSHLHK
KSKTSHNLTPPLSYSKNLPAJNLFEPTTSLSSPTSTIPDELEKESLISPLLPQDEIVNRQ
ENSPSHVDEVDENHYLNLADSLDSSYLHSHKHLGIENNLPRSNDLIDHLISDQIENNVMNLMFR
LSSS

YHR135C 2117bp CDS: 501..2117 public: 1..2117 (SEQ ID NO 701)

AGAATTAACGAGTACATTAATGAGAAAGATTCAAGTAGAGCGCAGCGTCAAAACCGTCGCCGCTTTT
AAGCAAGCTGCGCCATGACCTTTGGGAGAACGATGTCATTCAGAACACATATTCGAGATTCGCT
TGAACGAGAACATCATGATTCATCTCTTAATCGTTACATACATACCTTCTACTCTGATCTGTTA
CANATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC
TTCGTTTCTTACGATTTTTCGCGGGAACAGAAAAACAGAAACAAACAAACAAACAAACAAACAAAC
GGGCTTTGATTCCTGCTCTTTCATCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAA
GTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC
CTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
TAAACGAGAAACGCAATTTTAAACGTAACAGCAACAAACAAACAAACAAACAAACAAACAAACAAAC
CAAGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
CTTTCGCGCTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
TTATATATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
GAGATGAATTTTAAACATTAATTTCTGAATGCACTCCCAATATCCCTTACGCGATCTTACTTCGCGC
AAGAAGTTTTCGACATATCTTGTCTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
GTGGAAGAAATTTTCTGTCAAAACGCTTTCGCAATGCTGCTCTCTTTCGAGATTTATTTGATTCGCT
TGCAGGCAATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC
CTGACGCAAAACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC

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AGCAGATCCCATATAGAGAAAAAATCATCTACGCGGCTGCCAGATATATGCTCATTAATCTACAC
TTGGAAGAGAGCGAGTCCAGAAAGATATATAGAGAGCTTGGGTCACGTTTCTTTATTTCTTGAGAG
GCCATTCACCTGCGAGGTTTAAACCTCAACCAATAGCAAAATATGCAAAAGATTTGGAAGAA
AAAGATCTACTAACGTTTACGATCTTACTCTACAGGCTCTGTCGCAATGAGATATGTAAGATTCG
TCGAGATCTTCTCTTGAAGAGTGTCCGATTTATGAAAGCTATGAAAACTATCTATCTGTATCTG
ATCATTTAGGTGAAACCGCGAGCGGCAATATGATGATGATGATGATGATGATGATGATGATGATG
TTACATTAACCAAGAACCAACATTCATTCAGATTCAGGCAATTCATTCATTCATTCATTCATTCAT
ACATTAAGAAACCAACACTCCAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG
AGCATATGCTCTTAAACCTGAGCAATATGCGCAATTCCTATTAATTAACCAAGATTTAGACCTTAC
CTTATGAGCTTACCAACATTCATTCAGCAATATTCCTGAGAAACCAACCAAGAGAGAGAGAGAG
AAAACTTTCAGAGCAACATTCATTCAGCAACATTCATTCAGCAACATTCATTCAGCAACATTCAT
GTGCAACAGGCAACCTTCATTCATTCAGCAACATTCATTCAGCAACATTCATTCAGCAACATTCAT
ACCCACCAACCAACCTTCTGCTGCTTTCATTCAGCAACATTCATTCAGCAACATTCATTCAGCAAC
TAGCTGCTTCTCATTAAGGCTTTTCCAAAATTTAGTGTCTCTAA

YHR135C 538aa public: 1..538 (SEQ ID NO 702)

MSMFIATSTTLAVNLTNTINGANENVQANKQLHQAVDSPASSMTATTAANSNSRSDSTIVGLHY
KIGKIGBGRFVLEFEGNMINGVPAVLEFPRKTEAPOLRDEYKTYKILNGTNPVPAVYFQGEGLN
ILVLDLGPSTLEDFDMWGRFVSVTVVQVAVQMTLIEDLHAHDLIRKIPNPLIGRPEQPAANNI
HLIDFGAKQYRDPKTKOHIYREKRSLSGTARVMSINHLGHEOSRDMELGHPFVFLRGLHPWQ
GLKAPNNKQRYEIKERKSTNVVDLAGELPVQFGRVLEIVRSLSRECDRDEYGRKLLSLDLDGET
ADQGYDMKRLNDGMDININKPMLHGHGPNPPEKSKHNKRLQDMQDLQMLQ0000000000000000
TEADMRSQYFKLDPSTSEVAVQHTQKYLQEQQRQ000000000000000000000000000000
PSQYQAZQ050QFARVQPOQPSAALRPEQHPPNDNSLSAHSKGFOLGCG

YU1060W 1835bp CDS: 501..1835 public: 1..1835 (SEQ ID NO 703)

TAGACGAGATTTTGTAGATGATTTAGAGATTCAGACAGCTTCATCTTTCGATATTCCTTAATGT
AACGTAATCTGTTGATTAAGAAAGATGATTCAGAGAGATTAATTAATTAATTAATTAATTAATTA
ACGATGCGATTTATTCGCTCCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAAT
TTGATATCATCTTTCGCTCCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTA
CTGATATCATCTTTCGCTCCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTA
TTCGATATTCCTCCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AATATTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
ACAGAGATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TGGAGCTTTTGAACGCTGCGACAGAGATTAATTTTGAACGCTTTTGAACGCTTTTGAACGCTTTTGA
TCGAACTTTTGGTGTGAAGTTGTTTACGCTCCCAATTAATTCCTCAAGAGATTTGATTCAGAAATTA
CTAGAGGTGAAGATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
TCATTAATCAATTCCTCCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TACATTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
ACATTTGCGTCAAGCAACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC
CTTTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
AATTCGTTCTGCTCAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC
CAGCTAAGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TTACATTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
TTCAGATTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
ATTTCATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
TTGCAATTCATTCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
AAGAGACGCAAAAGCTGCTGAGAAATTTGTTAAGTTTTCAGTTTGAAGATGATGATTCATTCATTA
ATGCCGTGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT

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YJ060W 444aa public: 1..444 (SEO ID NO 704)

[illegible]

Y01.052C-A 61aa public: 1..61 (SEO ID NO 710)

YOL052C-A 61aa public: 1..61 (SEQ ID NO 710)

MEZITKA
add 188
CDS : 188-105
and 188-117
T89::T
(QES)
ON (T
/ 189/

Y01.099C 992b0 CPS: 501..992 public: 1..992 (SEO ID NO 711)

TGTCCAAATATGTTGAGATTCCTGTTTGGCAAAAGGGGGACAACTTCAATGAATGTGTAATTGGGAAGGT
 TGCAGAAATGTTTACCAAAACAGATCTGAATAATGCCATGCAGAAATATTTTGTCAACATATTTGATATCCCA
 AATAAAGGCTTGCTTTGTGAGCTGTCAATCCAGATTAATTTGGAAATCAGTTTCTTTTGGAAACTC
 ATATGCTTCACTCTCGAAATAGAGAGCTTAGAAGATGACGATGACGAATTTGATAGTGAAGAAGACGAA
 ATGGTGTAGTACATGACCTTCCATTTTCAGCTTCACCTTTTCAACACAGAAACAGTGCCTGATTTATCTGCAATTC
 ATATAATATGACAAAAGAGCAATGTCTCATTTTTCGAAATTTGGGATTTCTGCCTTACCGCGCTCTTTTC
 AATTGATTTGATCGAGATAATTAATTAATTTATATGATGACTTGTGAAATTCCTCATATATTAATTTATTTAG
 AGTATTAAGTGTGAGTGAATGAACATTAGATAAATTAATAATTCGACCTCTTCGATATTTTGCAGATG
 AGTTTGTGAAATATTTGTCTCTGTGTTTACAGCTTAATCCACGCTAACTGTCTTTTGGCAATCCGTTTAA
 CTAATTAATCTGCTTAACGGTACTTCGGTACGAGGCTTTTATTAATGAAATTTGTCTCTTGGCAATGTAAGAAG
 TTCCAAAATTTCTGCTCTGTTGCTTCTTAGCGCTTAATTAATCGATTCAGAAACAGAAATGTGATCTTTG
 AAATGTAGTGAAGATTTGGCTATGCGTCTCGGGTTTGGGGAAGGAGCACTTGGAAAGATCTTTTAG
 GTAATGGCTTTTCCGATGCAATGATGTCTTCTTTCATAATTTACCTTTTGTGTTTCTTTGCAACAGTTCCTTTCT
 CATATTTTATTTGATTTGAAATTAAGAAATTTTTTTTGGAGAACAGTAAACAAATTTTGTCTCTGGTGTTTTAT
 CAGTGTCTCAAAAGAAATGCATTTGTAA

VOL099C 163aa public: 1..163 (SEO ID NO 712)

YOL099C 163aa public: 1.163 (SEQ ID NO 712)
 MKTLQKINYYDLQFADEFLKFPVFRNPNTWTCFLGNPLTNLLVNGTGAACCFEFCSLALIKVSKILL
 DLLLLALLIDISENELCEGLDGMWLCVFGFGEDLVEVSGLWALPDDVDLLSITTFWFLCNSSFSILFVF
 FLLEFLRTVNNLLVFLFLVKRNDL

VOL1100W 3746bm CDS: 501 3746 public: 1 3746 (SEO ID NO 713)

[illegible]

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YJ060W 444aa public: 1..444 (SEO ID NO 704)

YJL060W 44aa public: 1..444 (SEQ ID NO 704)
MKQRFIRQKALDMSRPRKVKVQYFSTNSAKDWSLNTWEAAKNAANNSKNQRELINLGGFFSYP
QATEAKQALDIPWQYVSPGRRSLNLKLYSPINTLTKANVTWTGANEGLISCLMGLLNA
GDEIVPEFFPDQYTNIELCGKVVYPINPKELDQTRGEWITDEQFEKATISLTKAVILNTP
HNPIGKVFTRLELTNLGNICVKNVVIISDEVYEHLYFTDSFTRIALTSPEIGQLTWTGSAKSPFAAT
GWRIGTWLSLNAELLSYAAKATRICAFSPSPLOEACANSINDALKIGYPEKMRQEYINKFKITSIFD
ELGILPYTAPEGTYFVLVDPSKVKIIPEDYPYPEILNKGKDFRISHLWNLINELGVVAIPPTFEYIKEHKA
AENILRPAQCKDDAVLENAVERLKLKLDYL

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)

YKL123W 881bp CDS: 501-881 public: 1..881 (SEQ ID NO 705)
 AAAATTAATGGATGAACAATAATTCGCATTGATCTTCAATGAATATGGCGGTTTAATGGCCG
 ATATACAGAACAATATACAGAGGATGGCTATTGGAAGACATTCATGTTCCGTTGAAGCTCT
 CTCGAAGCGAAGATATTGAAGTCGCCAAGATCTCAAGAGAGTTACAGATCCAGATGAAGAAGTGG
 TGAATGACGCTCAGATAGCGTTGAAATTACATGTTAATTTGGGCCAAGTTCGGTTCGTTTATAGAAGC
 CAATGTGAAGAAATATGCTCTGGGAGTGTATTGGCCAAATTTGGBAATCTCTCTCGGTTATATGGAAC
 CGAGATCAAGAAGATACCTATTTTACAGAAAGAGGAAGAATGCCACAGATATGCCACATGATAA
 TTTCTTTGGTAGTAGAAGTTAAAGAAGGTCATCTCTAGAGATACGGCGGCAAACTAGTAAGCCCTT
 GTGTGCTTTGGGAGCTATGAAGAATCTCTCTAACTTACAGACAGAAATAATCTTACCGACGACAG
 TCTTTGAACCGGAGTAAACAACCCGATACCAATGATTTAATAACAAGATGAGAAGCGCTGTTCGACATGA
 AAATTCGCCCTATTGGAAGATATGGCAATAAAGACCGGAATAATCAAATCCCCCGGTGAAGATATC
 AGATGGAGCTATCAATACAGACCTAGAAATAATCTACTTAAGAAACGCTCAAGAAGACAGGCGAAATC
 TTTCAAAAGAAGAACAACGATCGAGAAAAATGAAGACATATATGAATTTGGTTTTTTTACAAATTTTACCGA
 TACCAATATACATCTCTGAGTTTTTTTTTCTTCAATTTCCATGCTTTTATG

YK1123W 126aa public: 1..126 (SEO ID NO 706)

YKJ123W 126aa public: 1..126 (SEQ ID NO 706)
 MKESLTLTTEKIMFTTTLVKPITITTTTTLITTTMRTLVAWKIRHYWQMAIKORKIIPVVKYQWELSI
 RPTVTNIIKKWKEETANIIKKRTRDRNKRHYEGFGFVNIIRHNIVYPTSTFEFFNSIV

VMR.028W 1091bn cns: 501...1091 public: 1...1091 (SEO ID NO 707)

YML028W 1091bp CDS: 501...1091 public: 1...1091 (SEQ ID NO 707)
 TGTAAACGATAGGGTGATAAACCGCTGTGTATAAAGACCTCTTTTGGTGTACACTACTCTCCCTCA
 TGGTAAAGAGAAAGCTGGATGATATGCTTGTGCACAGAGACGAGGACCGTGTAGCAACCGCTCCATCTGC
 CCAACAGCAGGAAGAACGAAGTATGAGCTCTCAATACTCTGCAGAGGAAGAACCCACGCCACAGGTGC
 GCAACCTCATCTCTACATTTCTGTATGAAGACTAATTCGAATCGATCTGGCCAGCTTATATAATCGGTT
 TAAAGGTGACAGAAACCCCATCTGTGTGGCCCTCGGGTTTGTGACAAATATGTCTCTTAGGAGATTGTT
 TCGGTTTGGCTCGGGTGAAGTACCGTGTGGCAACCAAGAGCACTCAACTCTTAAAGGCGAATATTCGT
 CAGATCAATGCCGAACCGTTCTCAACGGGCCCTTCCCTCGTTTCAATTTGCTCACAAACCAACCAACTAC
 ATACACATATATCAATCAATGATGGTGGCTCAAGTTCAAAAGCAGAGCTCAACTCTTTTAAAGAACTCTGCCTTAC
 TCGAGGCTGTCTTTGCAGGAAGTCTCTGTGCACAAATACAAGAGGTACAAGCTGTGTCCTTAGCCCTTTATTTTC
 CATTTGGCCCTTCACTTTTGTGCTGTGCACCAACCGAAATCATATGCTTTCTCAGAAGCTGCTAAGAAATTCGGAAG
 CAACAGGCGCTCAAGTTTGTGGCCCTCACTGACTCCGAATATCTCCTTTTGGCATGTGACCAATATCCC
 CAAGAAAGGAAGGTGGTTTGGGCCCAATCAACATTCAGTTTGGCGTGTACACCAACCACTCTTTGTGTCCA
 GAGACATATGTGTGTGTATGTGGAAGAAAGAGTGTGGCTGTGAGAGGTGTGTGTATCATCATCGAACCCCAAGAG
 GTGTCAATTAGACACATACCATTAACGATTTGCGGTGTGAGAACTGAGAAAGCTGTGTAGAGATTGG
 TTGAAGCCCTTCCAATGGACCGACAGAACGGTACTGTGTGGCCATGTAACTGTGAGACTGTGCTGTCTA
 CCATCTAAGCAGCCGTTGCAAGGATCTCCACAGGAATATTTGGAAGCTGTGCCCAACCAATAA

VMF028W 196aa public: 1..196 (SEO ID NO 708)

YML028W 196aa public: 1..196 (SEQ ID NO 708)
MVAQVQKQAPTEKKTAIVDGVDFDESLDKYKGVYLAFTPLAFTFCPTETIIAFSAEAAKFFEEQGAQV
LFASDTSEYSLLAWTNIPRKEGSGFNTINPLLATDHTNLSRDYGVGLIEEGVAALGFLIDPKGVYIRHI
TINDI EUCVCEWFAELRIEFAEAWMDKNGTIVPCNWTAPCAATLITPVDVDSKSEVFEAAK

VOL052C-A 686bm CDS: 501 686 public: 1 686 (SEO ID NO 709)

Y0L052C-A 686bp CDS: 501..686 public: 1.686 (SEQ ID NO 709)
TGGCCACTGAAATCTCTGGCAGACACCCCTGAGCTAAGGAGTATTAGCGCTCAAGCTTTTATTTC
CTCTGATCTAATATATACACACCCAGACAGGTGGCCAAAGGCTCGACGAAGCGGCTTCAAGAGGAC
GGGAGTGGGCTATCAGAAATACCTTATATATCATATATATTTTTCATCATCGCGAAGTGCACAAATC
AATAAGAGATGATGCTCAAAAGTTTATGCCCGATGTTCTCTAATGCCCTTCTCTCTAAATAAATACCT

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ACAGTTTACAGCATACGTTCGCATATTTTGGGCGTTGGATGTATGTAATTTCCAGATGATCCGCGGA
AACACCATTACAGCTACCAATATATCTTGACTTCCAAAGGTAATGTAAGTTCAGATACGCCGTTA
CACAGGTTTCCACTTATATACAGATTTTGGTTAAGAAATCTGTATTAATAAATCTAGACCCAGAT
TGACAGTACCCAAATTAAGGACATCATTTTTTCTAAGAAATTTGATTTTAAAGCGGCTCTGTTTGGT
CAAAAACGCCCTCCAGAGTCAAACCTATTAATATCAAGCCCAATCCATGACAGGCAATGCCAAGGGA
GCGATAGAAAATCTGGTAGAAATCTGCAATCCATTCGCAATCCATATGCTATCTACAGCTTACTG
CTTCAAGTCCCTCTGTGAAGAAATCTACATTCACCTCTTAATCAATATATCTACAGCTTACTG
AAAGTGAATTTCTATTAAGAAAGACCCTCATGATGAAGAAGACCGCAGATCTTGAATAATGCAAGA
AAGGTATTAACATTAAGAAAATTAACAACAGGCAAGAACCAAGTGGTGGCTTCTAGAGAAAGTAAACAT
CAGCTTCTGCTGCTTATTAACCAAGAACCATGCAAAAGCTATTCACACTTCTAGTGAAGAAAGTAAACAT
CAGCTCTCTCGGACACATCAACCAAGGAACTTAATAGGCTACTTCTCTAGAGAAAGTAAACAT
TTGCGCAATCTCCACCTTGTTCAGCTATGATTTATGCTAAATGCCAATGCCCTCATTACAGACCTC
CAATGTGGCCCCATATGACACCATATGATCAATCAATATGACATCCCTCTCTAGAGAAAGTAAACAT
ATTATTTCTGATATGCGCATATGCCGACTTAAGCTTGTATAGTAAAGAAATATGTTAAATATGACAG
ATTCTCCCTGTATGAACAAGCAAGATATTCATATGCTCTTATTCGAAAAACATCAACGACATGTAC
TAAGACCGGAAAACTGGAATTTTGTTCACCAAAATTAAGATATCTTGAAGAAAGAAATGCTTTAACTTAA
ATGGTTCATTTGTGATATCTCTCAAGTTGTTTGAAGCTTGAAGCTATGACTGTTATTTTCCAAAGAAATATAGT
GTGGGAGAGAGATTAACAGGTTTTCGAAATTTGACCTCTGGAAGATATATATCAATTTGAAGAGGTGACTTAT
ACTATTCGCAAAATATTTATTCGATTTTGAAGCTCTGGAAGATATATATCAATTTGAAGAGGTGACTTAT
CGGAGTTCCTTAATCAACGAAGCGGAAGAGGTACAATATGCAATCAAAACAGCTCACCAATATTAACCAAC
ATGATTAATTCGAATCTAACATTAAGAAAGCTCTGTTTCTTGTGCAAGATTTTAAAAAATTAATTAACCC
TCACTCTACGACGAATAACGCTCTCTTCTCTCTGATGAATAAAACCAAGTACTTAATTAAGAAACATGTGA
TGACATCAATTTGAAGAGTTTCTATGATTTCTGCAAGAGAGAGGCCCAATATCGATTACCAAAATTTAAAGT
TGTGACTATGAATATGACATAAATTTTTCGCTACACAGGTAACCAAAATTAAGAAACATATCTATCAATCCCTGG
TGTGACTATGAATATGACATAAATTTTTCGCTACACAGGTAACCAAAATTAAGAAACATATCTATCAATCCCTGG
AAATGGGAACCTAATCATATATGTTGATCTACAGACCTTACAGATCTATTTCTTTTGAAGCACTGATTAAGA
AAACCGACGAAGAAATTTGTTACTGTTCTTCAAAAATATCTTAATTTGGAATTAACAAATTAAGAAAG
AATCTTGCAAGAAACCAAAAGTATATGGAAGAAGAAACATCATATCTGGAAGAGCCATDACTTAAG
ATCTTCCAACTTCCAAATCTCTCTCTGCGCAAAACCCAGAGCGCATAGCAATCTCTCAATCAATTTCCAAAGC
ACAATGTGTTTCTGAATATGATTAATATAGCGCTGTAAGAGCAATGACAGAGATTTTGAACCTTTTA
CTAATTCGCAAGAGCAAAATTTCAAAAACAGCGCTCTCCAGATACCGTTAATCAGATTAATTAAGTTAAGC
GATTCGCAAAAAGACAAATTCACCTGCGATTTAGGCTTTAAACAAGAAACAAATTTTCAAAAACCTACCTG
CAAAATTCGAAGGTCCTTA

YOL100W 1081aa public: 1..1081 (SEQ ID NO 714)

IODIIONXSNPRLLRESDOEKUNILNLTTKKEXSHLDPHDAKATPQURSNRNVAGDLELEKFRAPKPI
 QALNTNDFIEYHNQORKNLDDDTKEVINDENKTAISTDGVADYDNDYNDINDQTKLNDIAGS
 PMHEKRNRYNVELEHDSVOXPIAKESKQAOIKIKIKIIOFKPESYGDAGSVTMLATSDITKRYAA
 ETCARYYAOIIDALDYHNGIITHDIRENILLDOBEKIKLUDFGAKLNTNNSVSPREYDLSIR
 KSVNATLKGSHLVDORASAPSVVEETHSTLYNNNTASTSELSIKRPPDERRAQILENARKGINRR
 KNOGCKRTBSGASALMAALAKTKMOSPTSSKSDSSSAPTSRPTCYKSTSTESKPFASXPP
 LASASTSKYKMPPEYTPMTPPYQTPTQYTPPTTKQSDYSDALAPRCSIKQVKNSTDSPLNNA
 KQDQMSFTYAKINENHVRPEKIDFETVNTYDILEKMKIKLNGSLDPLDLPKPRTFATFQVARSAGEVY
 KODIDFTMTAYSTEDDYYSKNIIDQLLEDYRIEGDSELLTMSGEGYKCONQNSPKMDOKSSSE
 NNKGSVSOKIKELIPMTSAELTSSDEKTKYKRIYATWTFERFLVFAKRPQPNVTMLKYLETIDT
 INDRQGTIKELIIPLEMGTINLVLOTPIKPSLTDWKTTSKLFVWLKINNSNTNKELELJÖRRN
 QVYIERTSTSGRAIPDLPFTNSKSPKPRKSSOPSISKNSFSEINSASKNBSNLIPEFTINAKEG
 NSKKHAAPEVPLTSKLVNGLEPKQYTVGLANTCTNFKNSASKRS

YOR302W 578bp CDS:501..578 public:1..578 (SEQ ID NO 715)

TCACCTTCGCGGAAAAAAGGCGATGACATGATATTTAAAGGCTCTCTCGTTAAGACATTAACTATGCC

131/251

AACGTCATTAGATTATTCGGTCGAATTCCTTTTTCAGGCCCTCCCTCTTCTCTTGTGACATC
GCGCTTCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTCAGAACTTACATACATACATTCGACAT
CTTAATCTTTTAAATCTCGCAAGAATACAGGTATTCGCTCTCTTCAATACCCTTTTSCAGATTGA
ATAATAAAACCATATTGTTTACCTTATTCGAACCTCTCAATACACCTCGCAAGATACANATTCAC
ACATCTGGAACCTAGCTCCCACTAA

YOR302W 25aa public: 1..25 (SEQ ID NO 716)

MFSLSNSQYTCQDYISDHIWKTSSH

138/251

TC TGC CAG A TA TA G A C A G A G T T G T C A A G A G G C C C A G H T T C A T A T A G A T T G G C A A G A G T G T G C
 AT T A C A C A T A T G A C A T T T G T G A G A G A T T C A C A A A C C G T G A A A A G G C C A A A C A A T T T G C A C A C A A G T
 G A A C A A G A T C A A A G T T C T T G T G A G A A T C A A A G C A A A A A A A A A G G C C A A A T T T G C A C A C T G A A
 G G G A G C C C A A T C A G A C A G A C A C T T G T T T C C A A A G C C A A G C T G G G A A T A G C G T A T T G A T A T C
 A A G A G A T T G A G G C A T T C A A G A C A A T T T G C A C A C A T T G G C C A C A C T A C C A C A A T T C A T T A T T A C T
 A A G A T T G G C C G C T G C G G C C A G A T T G A G C A C G C G T T C A A A A C T A T T A T T G T T G A A T A T T G C C G T T A A

YGR132C homolog 321aa (SEQ ID NO 428)

YGL313C_homolog_321aa(SsuU) (NC_067460)
 MGRIIDKIIISPPFSFSSFFSTSVSSPSLSLQNSMTSGRIADPFYSKALPAGITITALLAQSLAYDVF
 GGAARVAFIDRLKGVKQGVIGEGCHEFLPWVQKAVIFDVRVPRVLTITGSLQDNWLSLTIRVSRLEPVS
 RKLPITVQTGLDGERLPLPIGHEILKSLIYAQAEKALITQREVAEKLITQESLSRAAFENILEPVS
 ITTHMTFEREPYKAVEKQIQAQDAERSLIVLPRADAEKKAIIIRAECEASADVWSKALAGDGLLMI
 RLLEASKDIASTLSPNITLYLPNGAGGSDSDGSKNSLLNIGR

YGP135W homolog 756bp public: 1..756(SEQ ID NO 429)

YKRI35w_hm010g_r1200p_p42222.1 (1000bp)
ATGTCACGAAGAATGTCAGATTCAAGACACACTATTTTTCATCCAGAAAGTAAATTTACCAAGTGGAAATATTA
GCTTCACGAAGAGCATATTCACATCGATTACGAGCAGCAGGAGGATTTATTTCTCCGAAAGATGTCTCTTTTAAAGC
TGTCACAAAGAAAGTCACCTCCAGTTTATTTGACACATATGATCATGCTGAAATATATACATTTTATCTTAAAGC
GATCAATGATATTTGCGCTGCTGCTGATTTGATCTGCCGATGATCAATCTTTGTGTGAATATATGCAAGATTT
CAAGCCCAACAGATATTTGAAGTTGTACGACAGCAAGAAAGATCCCTCTGGATGATGTTGATTCATACCTGTTTGT
GATCTCAAAACAGATTTATCCCAACATGTGTGGTTGAGACATCTTTGGTTTATGTTTCCCTTATCGCGGG
TATGATGACAGATTCATATCCCAATGTTTGTTCATGGAATCCCTCTGGATTTTACAGTGGTGTGAAGGCGC
ACTGATATTTGGTGTCAACAATTTCTCTGCTCAAACTTTATGACAAAGATTAACAGACGATTTGAC
TTAAAAGATGATTCGATATGGCATCTCAAGGTTTATCAAAAATCTATGATCTTCAACATTAATAGC
GAAAATTTTGAATTCGATACCTATGATTTTGGCAAGACCAAAAGTGTTCATAAATTTTGAACGATGAAT
AAAGATTTTGACATCTCTAATTTAAGCTTCCTGGGGGTTTTGAACGAAAAAAATATGCGATGATGAATAG

YGB135W homolog 251aa (SEQ ID NO 430)

[illegible]

WCPR155W homolog 1491bp public: 1..1491(SEQ ID NO 431)

YERK155W_nucleotide_14930199_pos22251

ATGCAATATTCACAAACAAACACACCGCCCTTAAAGAGATATTTTGAAGACTATTTGGTAATATACCTCAATTA
GTCAATATTCACAAATTCACATAGATGTGGGAATATTAAGCCAGGCTATATGCAACCAATTGAATATATATC
AATGCGCGAGAGATCAATTAAAGATAGATATTCGCAAAATATATGCTATGGGAACCCCAAAACAAAGTATTA
ATCAACACAGGCTGATCTTATGATATTGAACCAACCTCAGGTAATATCTGTGTATTTGGTCTTGTGGTGGT
GCCCTTCCGGGATACAGAACCACTATTATCTCCAGCAAAAAATGTCAAAACGAAAGAAATTTCTGTATTTG
AAAGCTTAGAGATCTGAATATCATTAAGACTCCAACTGAAAGCTGACAGGAGACTCCAGATCTCTATTTG
GCTTATTCATGATAAAATTTGGAAATAAGAAATACCAACTCTATATTTTGGACCAATATGATGTAACCCACAC
AACCCAGATGCTCATATTAATATGATGCTGTTATGTAATTTGGGAACAACTGAAAGGTAATAATTTCTAC
TGTGCTCTGTGTCTGTGATCTGTGTGTACCACTACCTGTGATTTCAAACTGTGAAGAAATAAAATTTCT
AGATATCATCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
ACCGAAGGTACTATCTGTGTGAAGATATGTTATGTTATTTATTCACAGATGTTGTGAACGAAATATATTTT
ATGATATTGTGATCAAAACAGATGATGCTCAATCTTTTAATTTATGTTGTGTGAAGATATTTATGTGAAACAA
ATTATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TGATTAATCTTCAATGGAATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GAGAGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TGGTAACTCTTCAAGATTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GCCAAGCTTTGTGTGTATTTATTCACATCAATCAGGTGTGTGTATATGTGCACGATTTGTGTGTGTGTGTGT
TTAGTGTGTTTGAATCATCTTTATCCAAAGATTTGAATATCTTTAATAGATTAAGATTAACAGACCAAT
TCTATCATGTCGATCATATGATGATTTCAAAAGTTGCGCTGATTTTGAAGAAATCTTCAACATCACTAAAT
AATATCGAATTCACCTAAGAGAGTATTAATACAGATGATGAAATGAAACCAATGCTCAATATGTTCTAAG
TCTTTTGAACCAATTCAAATGCTTATTAACAGATGATGAAATGAAACCAATGCTCAATATGTTCTAAG
GTTCATTTGCTGTGTATTTGATCAAAAACCGTAGTTTAA

YGR155W homolog 496aa (SEQ ID NO 432)

YGH135W_Homo1og_4306aa[Seq. ID: no. 4321]
MSTNGTSGGADLEILGCTPLVAVKTKRTPQSLGSLAKAVYAKYLEFNAAGSISIKORIAKNWLVENEGQKQ
IKRGYTLIETPSNGTIGALIVGAVGRRITLPEMSEKISVLAKGLIELRTIPEAAMDSEKHS
GVAKLEKEIDPILSLIDQNGANPMDPAHYGCTGIEPMEQTEKTKTLVAGAGTGITGISYKLEKNS
KIVTGAADPKSGLIAPESPANSTEGYLVGIDYFDPVLRNRYXVDWIMTDAESFKLARRITREGG
ILVGGSSGSAIQALQAVAKDLTIEDTVVVVFPSPISRYLKFADENWLISNGFEVEDSPGANKADEFLNLT

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CKTIDLVAGKAPVYTVTLSPDVAKTFDLQSNCPDQLEVLNNSGRLVGLITLSKLKLSSTKKIQ¹⁰⁷TN
SISIIIDRRKLADEKPSFTTKKSGFTKRSEYETIKLDPLPLALNKFETNSNAIITDDEKLKPVQIVYTK
VDLSTYLTNNASF

VDLSYLTKNASF

YH138C homolog 384bp public: 1..384(SEQ ID NO 433)

[illegible]

YHR138C homolog 127aa (SEQ ID NO 434)

YHR138C_homolog 12/da13cy 10 no 3021
MNQNKLLGLILALISITTFNFKTISQTAIRSFVSFASSTATTNNTKSTMDSKGIITLKDTCAL
SEASSISKITELGKITNEFSLKGFSAQPTIHAEALPKDFAGIANIEEDGEVATQ

VHR179W homolog 1212bp public: 1..1212(SEQ ID NO 435)

YKHI 1/5W_Homolog 1424bp position 11322-11327
ATGCAACATGATCATGACAGGACAGTGTTCATTAAACCAATGCTG
CTTGCTGTTTACACCTTTACACAAAGAAATGCAATGCTGGTGTCA
CAAGAAATTTATTCGACCAATTTATTCGACCAATTTATTCGACCA
ATTTATTCCTTACGATTTTACATCAGAGTATTTATTCGACCAAT
ACATGACCACTTATCATCACTCATGAGGTGATTTGTCACATTTG
CAACCTTAAAGTTGGAAGAAATAATTAATTAATGCTATTCACAT
TCGATTTAGTGTAGTGTGCTATTCCTAAATAATTAATTAATTA
GAAAGAAAGTGTGAAATTTGGCCCAAGAAAGCTGGAAATCGTGC
GAGAAGAGATCATCATCATGTCGACATGTTGATTCGATATCAT
TTTGATTTATTCGACAGCTCATCTGTCATTCGTTGATTTATTA
AAAGAACTGATTAATTTGTTGTGTGCTGATTTGAAATTCGCTC
AAATTAATGCTATTTAGTGTGAGCTGAAATGATTAATGCTATTC
GTTGACGTGACAGGAAAGCAATGATTAATTAATGATTAATTAAT
AATGAATTTAGCGGTATTTCTCTGTGTGAACACAGGTCATCA
CAGGTGGCTCAATGATATTTATTTGAAACATTTGGAAGGGAAAG
CAGATGTTATTAATAATTTATGGAAGATTTAATTAATGATGAAC
ATTTCATTCCTGATTTAGGAAATAATTAATCAATGCGCATTTCT
TTTATTAATCATGATATTTTGGATTAATTAATCTGTGATTTAA
CAGAAGAAAGGAAATAATTTGGGTAAACCTTTAGCTTGA

YHP179W homology 403aa (SEO ID NO 436)

YKHH179w_homolog_403a3a10g_id no 1130
 YKHH162IVIKPLASTLSTQKIKGFFATLSORLAIKASTRYATKKNIPDLQLEYYSORSEYBETLLI
 TATYVTSROGLIYVYVGINDAQKQTSWKMINIYNAHNSAFSSVYQWGLYVNAFKILKDKGLPVGAS
 SYVWSEESKELAKANGELDEETFEEDILVEYEAIPAAKRALEADGYLEVSHASGLLQDLULANSS
 KRFDYKCGCSIKHARALLILIKLIDIVAGLERLALISPAFTQYANDKEDEIHSYIIDLQEPANGS
 INSLAYILVEROASLMDIADKENOVGSNEFLIKMKKRYIRACGYAVHKLNEEDINNDPRLIASFREF
 IINSPDLIKHLDGISTLYPERATYINDNFQNTWIKYGENKAFNEDEERKKLCKPLA

YTI,074C homolog 1392bp public: 1..1392(SEQ ID NO 43

[illegible]

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CAGATCCAAACAGTACTTTGGACCCAGCGTCCAGAGACGAGTATGCCAATGGGTGTTGGACGGCAAGATT
GATGATATGTTGGCACAATAATGCAAGGTTTGAGTATACTCTTTAGGAAAGTAG

YCR009C homolog 293aa (SEQ ID NO 524)

MKWKKKREFFCHSPFFFFLAHFFDLSMGWFKKANRAGASIVUKDVDTMDKDFDVEERYRYLT
 KTAGTNLQKAAGYLDNIRATINSQVTAIEITVLYEESKQSGSLXSNVCTYMQSVKPEDEETVKQID
 GPYRETVDLPDGTGFSNYFSEIDEATKKRAHKIDYEQCAKVRVUDVKPAKDAAKLPRASEKLSMAKEI
 YDELNDQKAEPLQILAIRVPPFFDSFEALVQLQAFECTEGYSRLAQIQVYLPDPSRDEYANGLLDGKI
 DDLMAQMGSLTSLGK

YCR010C homolog 858bp public: 1..858

1 CNUZC-Transcript 33369_F
 ATGCTAGCTGATTTAGAAATATCAAGAACACAAAGATCATCTATTATTGAAAAACAAGGGTGTATTAAC
 AGTAGCAACACACCAACACACCAACAACTATTAAGCTATTAAGCTTCATCTCAATCCATGTCAGTAA
 ATTGGAACACTGAGGAAATATCATTAATTTGGTAAATGAAGATTTATACGTTCTGATTAGTTCAGACGA
 TTTGGTGATCTTAATATCCAGGTTAGCTCCACACACTAAAATAGATTTTGGCTAAATCTGCTCCATTG
 GGAATATCCGCAATTTGCTTAAACAATTTGTTTAAGTTTAAATTAATTTGAAGCTAGAGGGGTATTT
 ATCTCTAATATTTGTTGGATTTGGCAATTTTCTATGTTGGTGCCTGCTCAATAGATTTTGGGGTCTGGG
 GAATTTGGCCGTTGGTAATATTTTGGTGGTGTGCTTTGGAGTTCTACGGAGAGATTTTGGGGTCTGGG
 GCTGCTATTTCAAGTTGATCAATTTGGTAATAAGCTGCTATTGCTAATAATACATCAAGAAATATCAATAT
 GCTGTGGGGAATATTTTAAATTTTGGTGGTTATTTTCCACATTTTCTTCTGATGCTTTTAAATCTT
 ACTGTGGCAATCTCTTTTAAATTTCTTTTAAAGTATACATTTTAAATTTAGGCAATTTCTGANTTT
 ACTGGTAAGTGGCAATTTAAAAAGCCGGTGGAGTGTGGTTTAAATCTGCTTTTGTGCTGTGGTATTT
 ATGCTTAAGTCGTGATTTAAATCTCTCAAAATAGTATTATTTACTGTTTAAAGCTATTTCCTACACGAT
 TTACCAATGCCAAGAAATATAA

YCR010C homolog 285aa (SEQ ID NO 526)

MSADLENOQPDHHLIENKGDNSNNHHNNNNSTSPYDHPHFITKLETGDGYTFGNERVLRSDLVER
FCGTLNGLAPPKPDNFANPAPLGLSAPALTTVLSLINCEARGVTPNTVWGLAFVGGAAQLVAGNF
ELAVGNTFGVALSSYGGPWGAAWAIQVDSFGIKAAAYANTEEHHYAVGLIGWFITFTFFMLLTWKS
TVAFLEIFFLSITFLLLAISDFTGKVALKKAGGVGLITAFVAVWYNAYAGIANPQNSYITVKAIPLDPA
LQDTRKONK

YCR021C homolog 1029bp public: 1..1029(SEQ ID NO 527)

ATGTCGCGCTGCTGTTCACACTTATCCGATATCATCAACAGTAAATGATGCTGTAAACGTGAACCCACCA
AACCCAAATATGAATATATCATATCAATCAAGCAATGGTAGTAAATGGCTTTGGGCTGTATTTTCAGTTT
GCAATATATGCAAAATGTCAGATGATCAATACAGATTTACTGAGCTTAGAAGATCATGGTTGAGAGAGA
GCTTTATTTGACTATACCCATATTTAATATGATGCTGTATTTGCCCTTGTCTTACTATCTATATGCTTCTAAC
TTGGGTACTACTTGTTGTTGACAGAAATCAACATGCTGGTACTGGTTTATGAGCAAAATCTTTATGACA
AAATTTGTGTCTGGTCTTGGTGTGGCCATACAGTCTGGTATTTTCCAAATATCTTAAACCAATACACG
TTTACTACTACTGAGATGAGTCTGATTTGCTTTAAGAAATCAATCTTCTTTGTTGTAAGCTTGTGTTACT
AGAGTTTGGCAAAATGAAGTTTCTGCTTTTGGGTATATATGATGGTGTCTTAAATGAATCTACTTACAAA
GGGGTATTTCAACTTTTCTGCTGTGTGTTCTCACTTATGATTTGCTATTTAGTCAATTAACCAATGGTGT
GTTTCATTTGGTTCATCTTCTCATTCACAGTCTTTTGGGCAATGCTCTTATCTCTTGTCTTTATGTTTGG
TTCTATGTTATTTGGATATGATCACTTTGGTGTATTTCCAAATTTATCTCACTTGAATGCCATTAATTA
AACGTTGATGAAGAAATCTTCCACCAAAATATGAGCAATTTCCAAATTTGAACAGAAATGAACATGCTCCA
ACTGCTACTGAAGATTTGAAAAGGATTTGGTGAACCCCAAGACATCTGGTGATGATCTGCTGTTCCT
CCCTACGTTGTCAGACACTGGTGTCTTCAAGCAACAGCCGCAAGCTGAAGATATATTTAA

YCR021C_homolog 342aa (SEQ ID NO 528)

MSAAVSTLSDIIRKDNVNNPNPILDIHTHSGDWLWAVSVPAFALVUHGTIVSYFTDVRKSGLKR
ALLTIPLENSAVFAAYTVASNLGYTWLTETNHAGTGRQIFAKVAFWFLGWPLVLAIFQITWTFS
VFTTDESDLLKGFSLSLFALFTRVLVAIEVFLGLLGLALIESYKNGVYFVAVFGLFAYLVLVNDVV
VFSSGSHSVHFLKALIFAIVTWILYPVAKWLEGGNVIQPDSKAVPGILDTLFGVIFPILTWIAININ
NVDEEFFFTKIMHPHLKPNENHATPYNDEKAVGCTPRHSGDTPAVPSGVPTGTGVQAQABAEERI

YDR178W_homolog 510bp public: 1..510(SEQ ID NO 529)

ATGATTTTCAACCTTTATTCACGTAATGGTGTAAACCACTTTAAATCAATCATCATCATCAATTAATCA
 ACTACTGTTGGACATATTAATATGGCCAAATTATTCAGAGGAATTAATAACTATTTCTCCACCAACAGT
 TATATTTTGTGACATTAATATGGCCAAATTATTCACCAACCAACCAATTAAGAAGGTCATATTCATAC
 TGGCACTAGTGAAGGAATGTTGCTATTTGGTATGTACCAATTAGTTTTAGCACCAATTTATTAATCTGSGTGT
 GGTCCTTCGACATTAATATGAATTCACCAATGTCAGCAATTTATTTATTCATGTCCACTGTTTGTCCAA
 AGGCTCTTATATAGATGATTTTCAACAGAGTTTATGGACTTATATTAATTTATGTCATCATTTATTTG
 TGGTCTTATATGATGATTTTCAACAGAGTTTATGGACTTATATTAATTTATGTCATCATTTATTTG

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ACTTTGGTACTGGTATTGCTGGTTATGGTATTTATCTAAATTGAAACTAAAGAAAGGTGGTGTGTTTCCAAAT
ATTATTTCAAAACCTTTGGAAAGCTTAA

YDR178W_homolog 169aa (SEQ ID NO 530)

#BXNDZCZ#
MISTYRIGLTTLTCKSSSSSLTTPVRLLLANFRGIKTIQPPGYIVGTVDAYVPPPCHKLEGLSH
WTSERIVAIGMLPLVLAPPTGGGASTLDSTMSALLLFHCHTFQSCIIDIPKRVGYSYHNMYALL
TCTGAGYGTYOETKEGVSNII SKLWK

YDR202C homolog 387bp CDS: 1..>387 public: 1..387 (SEQ ID NO 531)

12056221001027 500 bp

ATGACGCAAAATCTTGGAAATATAAACAATTCATAGATACATCTGTATATTCATCAATCAATCAACTCAAAAT
GTAAAGAACTTCAATTTGGTATATTAATTAATTAATTTAAATCCGATTTACTTCAAGTAGACATTTTA
CAGATTTGTTCAATTTGATGTTGATGTAACAATTAACACACAAAGCACTGATCTCAAAACAATCTGTAAGAAA
GGTCAATCTATCAAGCTACCTTTGTCTTTTAAACCAATCAACAGATCTCTCAATGGGATTAATAACCCGA
GATGGACCATCAATCAACAGATCTTAAATTTGACGGTTTGAAGATCTTATTTTCAACACGACATTTTCATTAAG
TTGCGCTTAAATAAGACCAATGGTTTATTTAGAACCTTTTAAAT

YDR202C homolog 129aa (SEQ ID NO 532)

MTANLNKTKFIDTVLSIQSTQNDKELHWYIINIILPDLPIIETLQICSNLLMYNSQPEPDSKQCIK
GPSIKLPLSLTNOODSVGIITRDGPYITDLNLTVKNNHYFNKHFHKLRLIKPMVLEQLVN

YDR256C_homolog 1458bp public: 1..1458(SEQ ID NO 533)

ATGGCTCTCAACATTTACGAATCTTAACGGTCAACCAATTCAGAACCACTATTGCCACTCAAGAAGTGTGT
CAACACGGTCCAACTTTGTCACAGATTTCAATCTTGAATTTCAATTTGCCCATTTTCGATTCAGAGAAGA
ATCCACAGAAGAGTTGTCACACGTAAAGTTCCGGTGCTTATGTGCTTTTGTGAAGTCTACTGACAGCATTC
ACTGATATTGTGTCGCCAAATCTTTGGACACTGTTTGGTAAGAAAATCTAGAAATCTTCTCCACAGATCTCT
ACTCTGTGTGTGAATATAGTTTGTCTGCTAGACTGCTAGAGATCTCAAGAGAGTTTGTCTCAAAATTTTAC
CTCAAGAAAGTATCTTCGATTTGGTATTACAACTCACTCAGTGTGTTTCTTACAGACCCCATCTAA
TTCCACATTTATCTCAACCCAAAAGAAACCCAGAAATCTCATTTGAAGGATGCTAACATGTTTGTGG
GATTTACTTGACTCAGCAATAGAAATCTCAATCAAGTTATGTGTTTATCTCCGACAGGTGACTCCCA
GCTTTTACAGAGAAATGATATGGTTTCTTGTCACTTATAATATGCTCCAAACAAAAGGTGAATGGT
TTTATTCGTTCAAGTTCAATTCATCTAGTACCAAGATATTAGAATCTTGACACAAAGAAGCTGTGTGCT
TTAGCTGGAATCTCAACCCAGTAAAGATTTGTCTCAAGAAATCTGCTGTGTAACCTACCCCA
TCATGGAAGTCTTACATTCAAACATGACTTAAGCCGAGCTTAAGAAAGCTGAAATTTCTTGTTGTAT
TTGACAGATTTGGCCCAACAGATATCCCATTTAGAAAGATTTGTGTAAGTTTCAATTTGAATGAAGAA
CCAAAGAACTACTTTGTGTAAGTTCGAACAGAGCTGCTTTCTCTCCAGCCCAACTGTTCTTTACATGGAA
CCATCTGCTGATTCAGTCTGCAATATGTTTCTCTTCTGCTGATTACTTCACACACACAGATTTGGGT
ACCAATCTACTCAATCCCAAGTAACTCTCTCCCGTGTATTCTTCAACCACTATATGAGAGAT
GGTGCTATGAGCTGTTAAATGTAATCTTTGGTAGCCATCCAAATCTCTGCGCACTGATTAAGCCAGTTCGA
TTTCAACACATTTTCTTCAAGAACCAAGATTTGGAATGGTGTCTGCCACTTCCATCTCCACTGGGAAA
GCCACCCAGCTTTTCAAAACAGCTCAAGAAATCTGTTGTAAGAGATATCCAAACCTCAACCAACAA
GAACATTTGGCCCCAACATGCTCTAGATGCTGCTGGTGTGATGCTGCTATTCCAAGACAGACAGTGT
GATPACTTTTGTAAAGTCTCTCAAGACTTGGCTGATGCTATCAAAAAGGAAGTTTGTGGAAATTTATCTTCCA
ACAAATAA

YDR256C_homolog 485aa (SEQ ID NO 534)

MAPPTNSNGQPIPEPPAQVRQGMHLLQDFNLIDSLAHFDRENI PERUVHAKSGGAVGVFEVTDI
 DICAALFDRVQKXKTRITFRFSTVGELSGADTADPRGFAKFTVEGNLDVNYNTVFFVTRDSEK
 PPIEIHQKTRPETHLKDANFMWYLTNSNEESIHQWVLFSDRGTPASVREMGYSCHTHTVSKNKGEM
 FVYOVHFTSDQGIKTLTWEEAGALAGSNPDVAQEDLFKNIAAGNYFSWTAIOTITTEABEAKAEZFSVFD
 LTKWPHKKYPLZFRFGKTLNENPKNYAEVEQAAZSPAHVTPVMEPSADPVLQSRLSFYADTHRRHLG
 TNYQPIPVNCZPLRFGPHMDKGMATVNGVLSGSHENYLASDKPVEFGQLQEDQVNMWAAFPFHWK
 ATPADFKQAQELMWKVLKRYPNQQEHLAHNIVHAAGADAAIIODRVFAFGVKVQDQLADAIKKEVLELSP
 RK

YER103W_homolog 1971bp public: 1..1971(SEQ ID NO 535)

[illegible]

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YMR035w_homolog 373aa (SEQ ID NO 570)

MTSLTEQDTALAKYLELSQNSKILAEIYWIIDAEQNTSKCRLLSKRPVSVDLPENMYDSSSTQAPG
HDSIVLPVAFVPPFPRKDNIIIVLNECMNDGPNKHNREKCALMKHABSEVWFGLQETVLEFD
QYDVPYPMKRGFPAPQGFVPGVGIVGVAVDIVIAHVAHNDVETAGINISINAEVWFQVPE
GIEGDDLMIAHYLLQRAVEEPAVKISHPKPLKEMNGAGCHTNSTKSRIVGGMKVIISALSLAK
RKHEHMLYGADNDRLRGHEHNDTSSSVANRGAIRIPROVAKEGYEDREDRPASNIDPLVLT
GIWETICGSLPDADMAKEFLRESSDNN

YMR099C_homolog 900bp public: 1..900 (SEQ ID NO 571)

ATGCGAGTGAAGAGCTTGAAGACGCTGTATTCATCTATGATCCAAATGATCAATACAGAGCCACC
ATTGTGAATTTGGTGTCTATCTGATGTTCTTGGAAAAACAATATCAAGAAAAATGGGTATAGAA
GGTCTCATTTAGATGGAAGTAAAGCCGTAGAGGTGATATCCATTATGTTTCCAGTTTCGGTAAA
CAAAAGATCAATATCATCCAGCTTCAATATCTCCACATGATGATGTTGCTTACACTTGGGAA
TTCTTGGGACAACCTCAAGAAAGTCCATATGCGGTCAATTTGGAATTAGGTCAGAAAAATGTATCCA
GAACTTGAATTTAGATTAATGATTAATGATTAATGATTAATTTAACTGTATGTTAGTTCAAGATTAATG
GTATCTTCAATGAGGTGGAAGAAACCTGGTGAAGAGCAATTTGAATTTATGTTGTGTGTCATACATAT
TATAGATTCATGATCAACCGATATCATTTGTTCCAAATTTAATGACCAAGATTTGATAGATTTATCA
AATGCTGATTCATATATGGAAGGAACAGTTATGTTTCCATGAAAGAAATTTGATAGATTTATCA
AAAGCTATTTGGAAAAATCCATTCAGTTCAGTGAATTAAGGTCAAGTCTTTCATCTCATGAAAA
AAGTCCCTGATTCCTGTGTATGGAATCCATGAGCTAAAGCTGAATGTTAACTCAATGCTTTTACAGCT
AATACGAGGTTCATCAAAATGCTGTGTGAGCCAGGTCAATGTTAACTCAATGCTTTTACAGCT
GGTGGAAATGTGTGAGGTGTCAAGAAATCATATTTGCGGTGAGATTAAAGTTCAAGCTAATATTAT
TAG

YMR099C_homolog 299aa (SEQ ID NO 572)

MPVELEDEVLITDPDSTNSTRATILKEGATVTVSWNSNQEKMLSEGAHLDSKAVRGIPLVFVFGK
QKDSHVPFPLKFOHGRPNRSTWFEFLQGTQSPITVQGLGRENDDPELTKLXNVOPTLLIVNLTADKL
VTSIDVENTGKAEFENMFLFHTYRLHDITDVLNLIIDQCYQLIGESTIERAPVTSFHEFEDTYS
KVSLEKSIQVVRKGOVLFNLHRKMLPSVWNPWTKRAEGHADPQKSGFHQMVCEPQHVNSMVSILPA
GKRSKSGGEITTTGGELKIVQANIT

YBL085w_homolog 3519bp public: 1..3519 (SEQ ID NO 573)

ATGATGGGGGAGTACTTATATATGATTAATAAACAATTAATGCGAGTTAGCGCATGATTAAGTCTT
AAAAATGGGACAAAAATTCAGATATGCTGACAGATAGAAATATATATGATGCTTGTGATCATGGGAAA
AACTGTTGAGGAGAGAGAGGCTTATATCCAAAAACATTTACATTAATTAACCAACAAATGATG
AAACATCTTATATGATCGAGGTCAAGAAAGAATGATGCGATTAAGGTTCCGAAAGAAACACCA
AAGACACCATCATCCCTGTGTGTGATGATTCATTCACACATCTCTCCAAATTTCCCTCCAA
TTGTCATCTCAATCAAGACATCTCCATTTAGCTGACCAATATGTCAGTGAATTAATTAATTAATGATTC
CAATCTTCCATATATGCTGGTCTCATTTGAAAGAGCAAAATTTGATGAGATTAACATTAAGAGG
CTATATGCCGACTTGAACCAATTCCTGGCAATGTTTATATGAGACAGAAACCAACACATTAACAC
ACTAATTAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT
TCGAAGAAATCAAAATGATATGCTTCAATATGATCAATATCAATATCAATATCCCAACCAAAATAT
TTGATGTGAGATTAATCTGCAATATCTTTAATCTGACATTTGGACCTTTGGAAGCAATATCTTGACA
TTCAGTGTGAGATTAATCTGCAATATCTTTAATCTGACATTTGGACCTTTGGAAGCAATATCTTGACA
CAACCAAAATCATCTGGAGAAATCTTGTGCTGTGTGATTTGAGGTTGATGATGATGATGATGATGAT
TCATTTGTTGATCCAGTTCAATATTAATTAAGAAATTTGGGAAATTAAGAAATTTGAATTAACGAAAGAT
AAAGATTAACATTTGAGAAAGATTTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT
GCAATTAATATTCACCAACATGATTAATGATTTTCCATGATTAATGATTAATGATTAATGATTAATGAT
ATGTTTAATTAATATCTGGCAACCAACAAACAGACATTAATGCGATACGCGTTTGTGACCAATCTGAC
TTCAATTAATTAATATGTCACCAACAAAGTGTCTCAATATCATCAAGAAAGATGATCATCTGATGAT
GTGACCCCAACAAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTGTGTGAGAGCCCAATTTGATTAAGTTTAATTTGGTGTGGAAGCAATGATTAATGATTAATGATTAAT
CACTATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTATGAGAGAGCTGATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAACACACACCAAGAGAAATTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAACATCATCAAGAGCTGATCTTCTCGGTATTTCTATACCTTTCTGCTGTGATTAATGATGATGCGCAAAA
CCACACCAAAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GAGATTTTACTTCTTCAAGCAATTAACAAACAAATTAATGATGATGATGATGATGATGATGATGATGAT
AGAGAACCACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTTGAATTTTCAATTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCAGTTTCCGACCAAGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACAGGATTTGATGATCAATCAAACTTATATATTCATCAAGATTAAGGATTCCTGCGCACGTCACATCA

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AGTTTCCGAAGTTTAAACAGGGTCCAGAGAAACAGAAACATCAGCATTTTCAAGAGGTATACGTGAGATT
ACTCTCGATGACGCCATTTAAATCTGCCGCTCATAGTGGTTATATGCTTAAACGTTAAATCAATTTA
AGCTCGATGACGCCATTTAAATCTGCCGCTCATAGTGGTTATATGCTTAAATCAATTTTCAATCTTTGA
AGGAAAAAGGTTGATTTGATATTTGATATTTGATATTTGATATTTGATATTTGATATTTGATATTTGAT
GATTAAGCTGATATATATGCTGCGATGATGATGCTCGACAACTTGTGCTGATATTTGATTTTGAATG
GTTCCACCGCTCCAGGTTTAAAGGGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTT
GAAACAGAAAGAAAGAGAGCTTGAAGCAATGATTAATCAGCAACCCATTAATGATTAATGATTAATG
GTTCTGTTGTGATGATGTTTCTTATCCCAACTGTGATGTTTAAATGATGATTAATGATGATGATGATGAT
GCCAGAGAGAAACCAATTAACAGATTAACATTAAGATTAATGATGATGATGATGATGATGATGATGAT
ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACTTCTTCAGTGAAGCACTTCAAGCTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT
GGAACATGAGATCAACAGGGGACATTAAGTATCCAGCAACATCAGTGTGATCGGTACCAACAAACCA
GGAACATGAGATCAACAGGGGACATTAAGTATCCAGCAACATCAGTGTGATCGGTACCAACAAACCA
TCAACCAATTCAGAGAGTGTGCTGCTCCAGAGGATTTGATATTTGATGATGATGATGATGATGATGAT
GGACCTTTAAGAAATTTCACTTCAATTCAGATATTTTGTGATATTTACTTATTAAGTTTAAAGTTAA
CCATCTTCAGAAATTTCCCAATATGCAATGCAATCACTATGATGATGATGATGATGATGATGATGATGAT
TCCAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCCATCTCAATTTCTATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ACCAACCAACAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TCTGTCACCAACGAAACAAACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GATTAATATGTTGATGATTTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT

YBL085w_homolog 1172aa (SEQ ID NO 574)

MDGDIYCIKQFNARLDELISLKGDKQVLAADREYNDGWTMKNLJLGEAGLYPKPTQLITNNDS
KTLRSRSMMAKPSDQETTPKDTTTPVSSNLNPNTPNPPTPLSSSTEPHLEPMSQLANKDS
OSSQYSHSINSOIDRALOELGNSADILNCGSEFENHNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
SKTSNDSLSQYQYQSLQDQPHLSDGSKRSQSLDLDLQKANTWMPKQVSSYVALVGLFDPMDVGFAP
OHITGELIELDELDELDELDELDELDELDELDELDELDELDELDELDELDELDELDELDELDELDEL
LANSPASTATLHDVAPPHLIDNNMNTNGKQOQLMPASVLNMTSDVNNNSQOQSGNHHOKRSSVD
VAPQOYIASDSTWSPRAPQPPSESPSIDTYSYKAGSEYDPPSHYGMATRTGNSASHLSSSPGI
NSPSPASSIYDSFSNNHNRGSSYKQHHNRNNSVTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
PTPLLSKTFQSNLKYGGDHDGDTFTSSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
FDLSNSPVDIDDAKPSPKNSVSUSTRKSDMALNGNDRVRVSDSTGSLSQSKPNSSRLKQIRATSYQ
SFLSLNDSKSKSTAFQGRITETPDEALIKTJSHSYMSKRSNNNLAMRRYFTLHGRLTSPQSLKDK
KEGLDITTAHKLVIPIEDASDPTDADRYAAVASTFAGENCYFLKVPAPVFGFKGLTQKRYTHFVAV
ETREEMAMVWYALMOATDIDSDVPSCTPTVSLNKAQOELATKAELEKLTDEQLKANYGIRLEED
INDTSFASLADYPDMSGDIPTGSTSPVAATSAKPLLDNPNKRSCTGMGTGTGTGTGTGTGTGTGT
QIPRSSQSGGFASGGLYLSGLLSPKSGGAGPVGIVSSSPINENGPPLRNSTNISEYFGDITVYSLEK
PSRQNSOYASITSGGSLIGFYGGLGSPATLIGGGGGLVSTSTPSTGSGTSSNMYNNNNNN
NNNNNNNSPINEPSSSDLKSSSPTTTTGTSTSGSKRQSRSTSDKMLGFSDSAQSHFTVIRKKK

YBR019C_homolog 2028bp public: 1..2028 (SEQ ID NO 575)

ATGCAAAACGAATATATCTTGTACTGCGGCGAGGTACATGAGTTAGTGTCTCATACGTTATGGAATTA
ATCGATATGATGATATATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
ATTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
AAAGTTTCCAAAGATTAATTAAGATCTGAGATCATTTCAATGATGATGATGATGATGATGATGATGAT
ACAAAATCTCCCTTACGATATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA
GCCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TTCTATTTAGTGTATTTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT
TATTTAAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TTATTTACTTATTTTGGCTTAAAGTGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT
AATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
GATGTGCGGATTTTGAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTT
GATTCACGTTTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGGAAAGACGTTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
TGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
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[illegible]

[illegible][illegible]

206/251

[illegible]

207/251

[illegible]

[illegible]

[illegible][illegible]

233/251

YHR135C_homolog 1488 bp public: 1..1488 (SEQ ID NO 721)
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YJL060W_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)

YJL060W_homolog 1362 bp public: 1..1362 (SEQ ID NO 723)
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YEL032W_homolog 2637 bp public: 1..2637 (SEQ ID NO 719)
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 TCTTTCAAAACGGTTTCTTATGATTTCTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT
 CAAGAAAGTTTAACTGATCAAGATATTAAGATATTAATTAATTAATTAATTAATTAATTAATTAATTA
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 CTCTTTGTTGTTGATGATGTCACCCCAAGAGAGAGGCTTATTTGTTGTTGTTGTTGTTGTTGTTGTTG
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YEL032W_homolog 878 aa public: 1..878 (SEQ ID NO 720)

YEL032W_homolog 878 aa public: 1..878 (SEQ ID NO 720)
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YUJ060W_homolog 453 aa public: 1..453 (SEQ ID NO 724)
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VINPNHPHIGKVFTEKELIKGLAEVHNLIVSDEVYENLYYDIDKPRPALPOLPELAEURLYVGS
KSEFAATGWRVYIOGPANLLEKVTIAHRLICSTPRALQQAIVSGFQDAESNFEINRKEYEHKIK
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YML028W_homolog 591 bp public: 1..591 (SEQ ID NO 725)

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YML028W_homolog 196 aa public: 1..196 (SEQ ID NO 726)

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YOL100W_homolog 2835 bp public: 1..2835 (SEQ ID NO 727)

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YUL166W_homolog 288bp Pathoseq: 1..288 (SEQ ID NO 729)

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YUL166W_homolog 95aa Pathoseq: 1..95 (SEQ ID NO 730)

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YLR038C_homolog 252bp Pathoseq: 1..252 (SEQ ID NO 731)

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YLR038C_homolog 83aa Pathoseq: 1..83 (SEQ ID NO 732)

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Figure 3 - 1

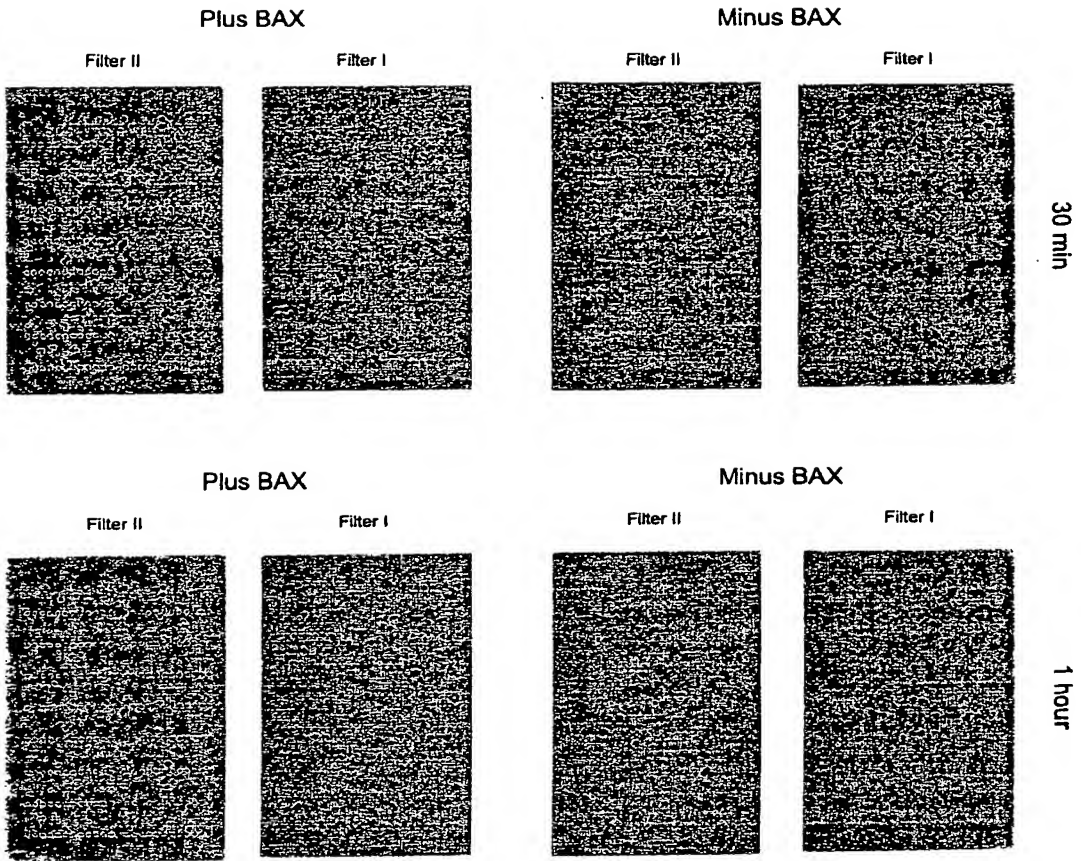
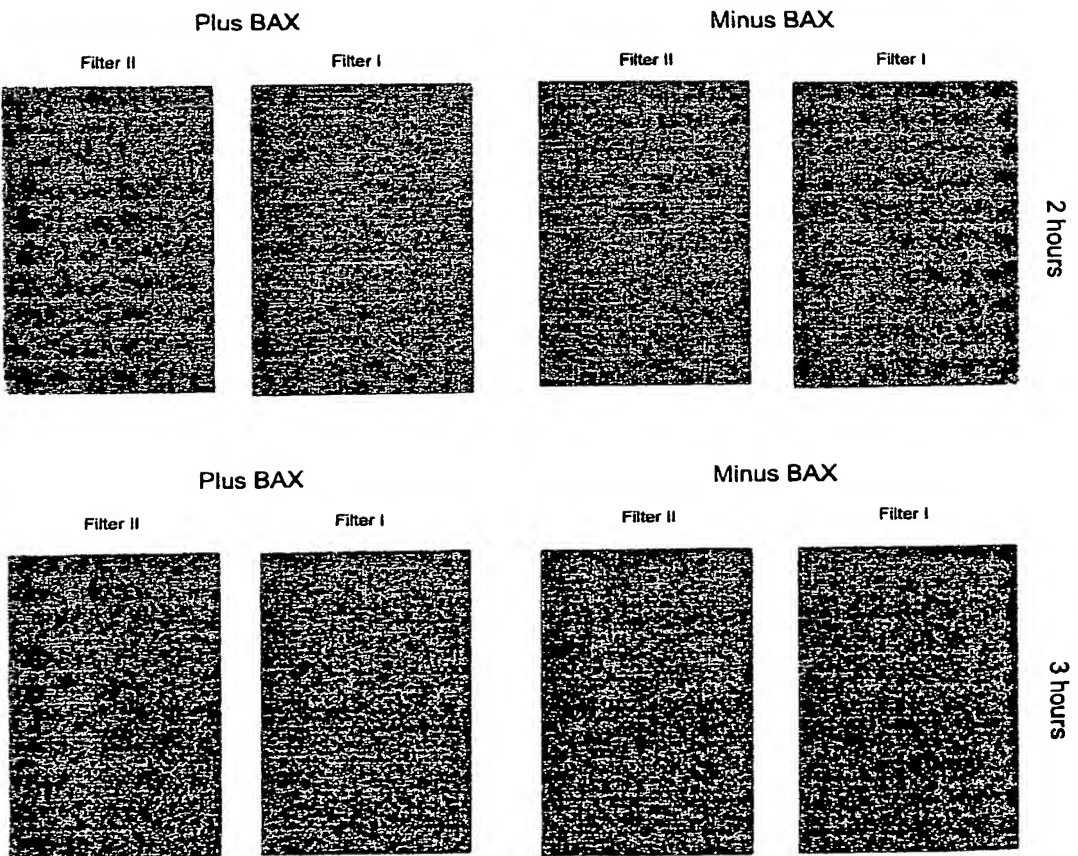


Figure 3 - 2



6 hours

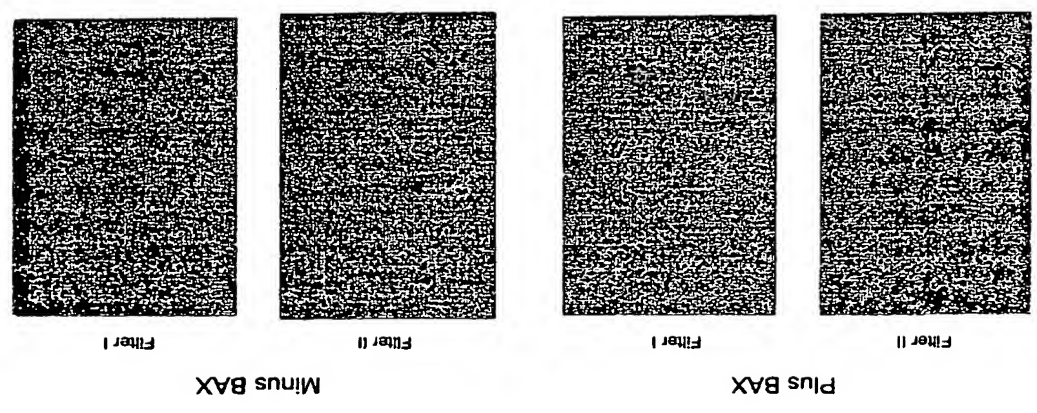


Figure 3 - 3

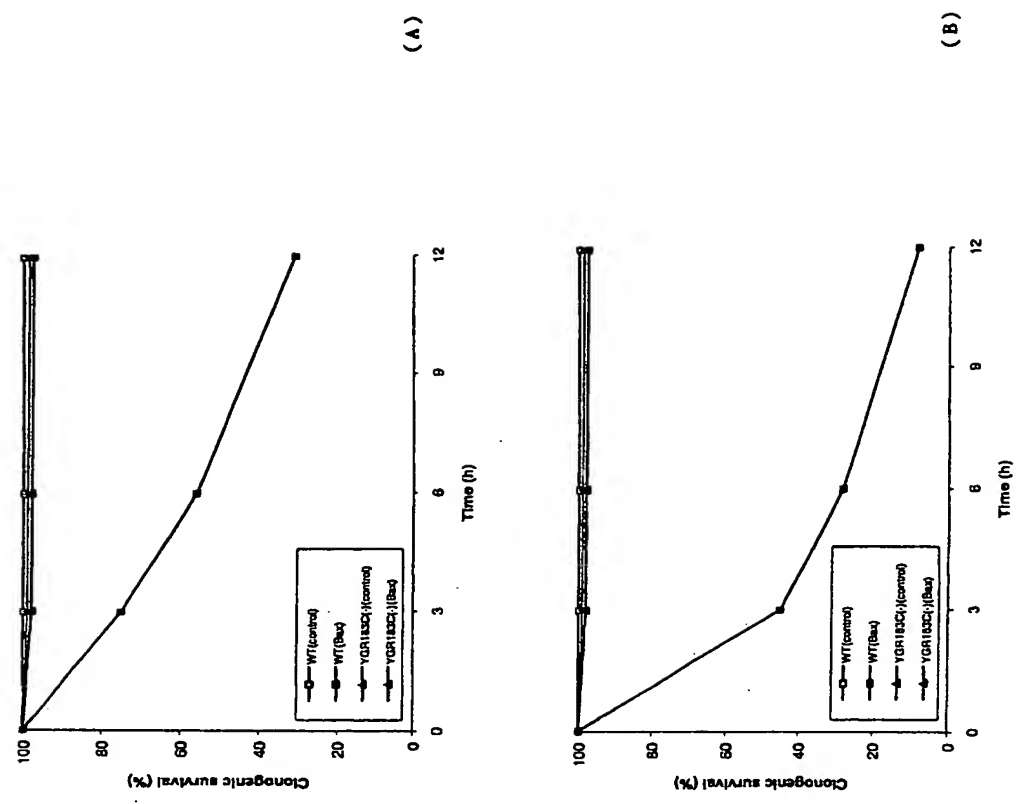


Figure 4

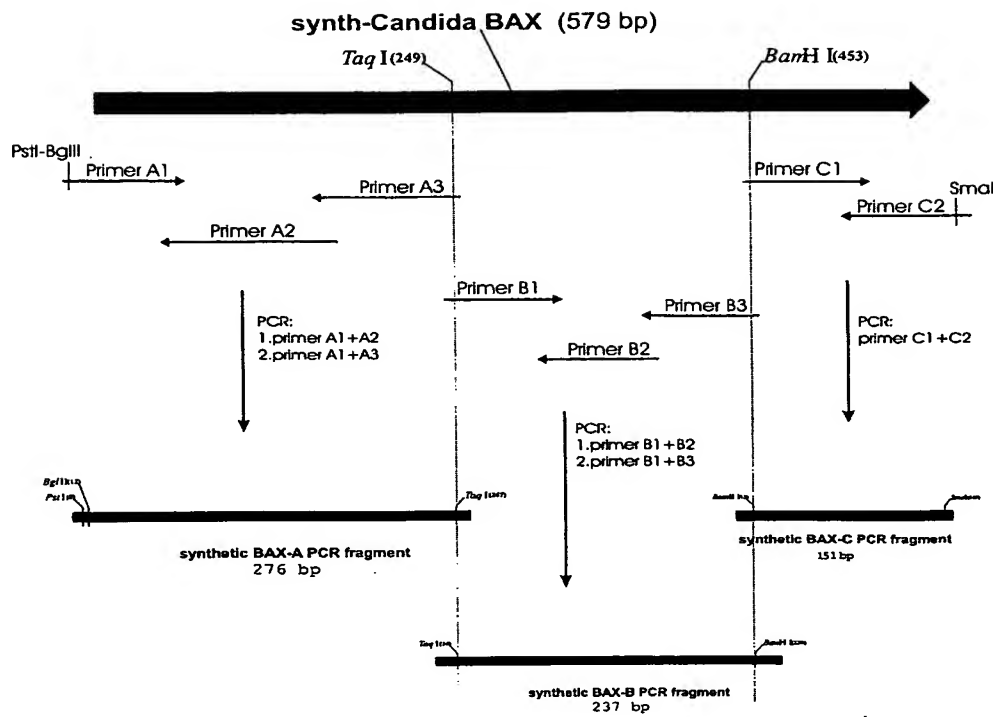


Fig. 5

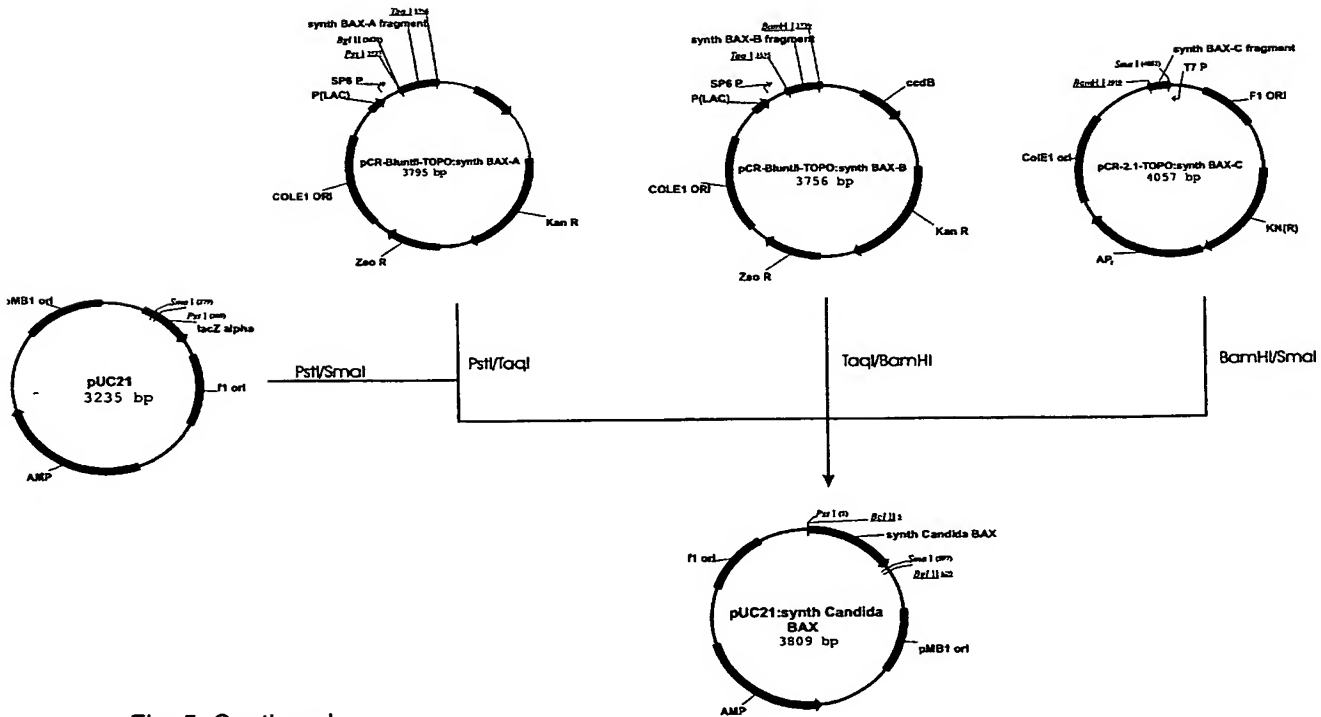


Fig. 5. Continued

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61 AAA ACC GGT GCT TTC TTG CAA GGT TTC ATC CAA GAT AGA GCT GGT AGA ATG GCT GGT
Glu Thr Pro Glu Leu Thr Leu Glu Gln Pro Pro Gln Asp Ala Ser Thr Lys Lys Leu Ser
121 GAA ACC CCA GAA TTG ACC TTG GAA CAA CCA CCA GAT GCT TCT ACC AAA AAA TTG TCT
Glu Cys Leu Arg Arg Ile Gly Asp Glu Leu Asp Ser Asn Met Glu Leu Gln Arg Met Ile
181 GAA TCT TTG AGA AGA ATC GGT GAT GAA TTG GAT TCT AAC ATG GAA TTG CAA AGA ATG ATC
Ala Asp Val Asp Thr Asp Ser Pro Arg Glu Val Phe Phe Arg Val Ala Ala Asp Met Phe
241 GCT GAT GTC GAT ACC GAT TCT CCA AGA GAA GTC TTC AGA GTC GCT GAT ATG TTC
Ala Asp Gly Asn Phe Asn Trp Gly Arg Val Val Ala Leu Phe Tyr Phe Ala Ser Lys Leu
301 GCT GAT GCT AAC TTC AAC TGG GGT AGA GTC GTC GCT TTC TTC TAC TTC GCT TCT AAA TTG
Val Leu Lys Ala Leu Cys Thr Lys Val Pro Glu Leu Ile Arg Thr Ile Met Gly Trp Thr
361 GTC TTG AAA GCT TTG TGT ACC AAA GTC CCA GAA TTG ATC AGA ACC ATC ATG GGT TGG ACC
Leu Asp Phe Leu Arg Glu Arg Leu Leu Val Trp Ile Gln Asp Gln Gly Gly Trp Glu Gly
421 TTG GAT TTC TTG AGA GAA AGA TTG TTG GTC TGG ATC CAA GAT CAA GGT GGT TGG GAA GGT
Leu Leu Ser Tyr Phe Gly Thr Pro Thr Trp Gln Thr Val Thr Ile Phe Val Ala Gly Val
481 TTG TTG TCT TAC TTC GGT ACC CCA ACC TGG CAA ACC GTC ACC ATC TTC GTC GCT GGT GTC
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541 TTG ACC GCT TCT TTG ACC ATC TGG AAA AAA ATG GGT TAA (SEQ ID NO 1)

B

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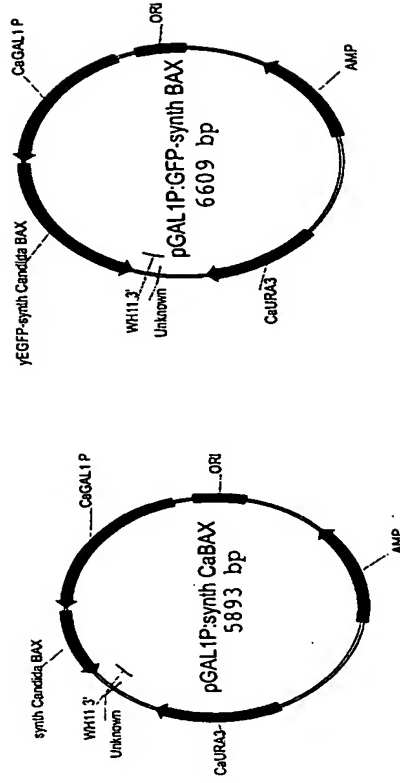


Fig. 7.

Fig. 6

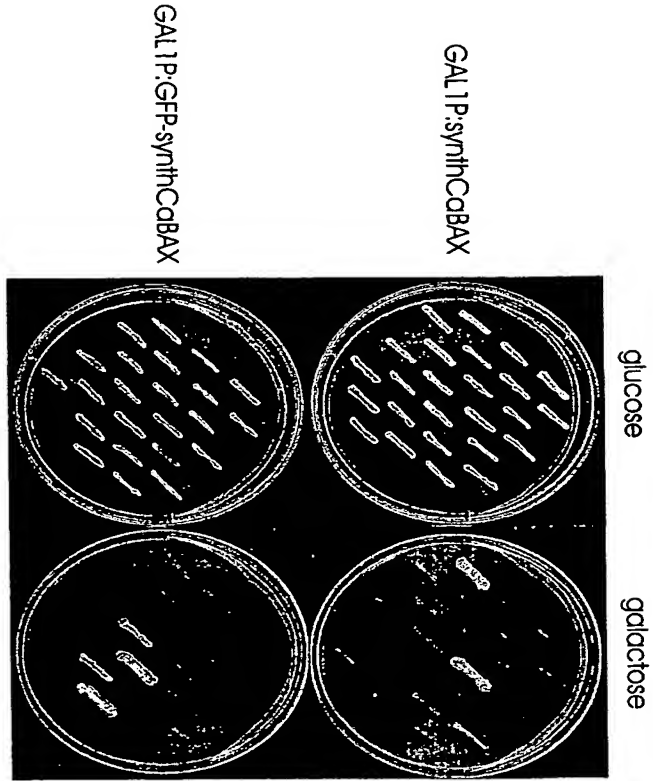


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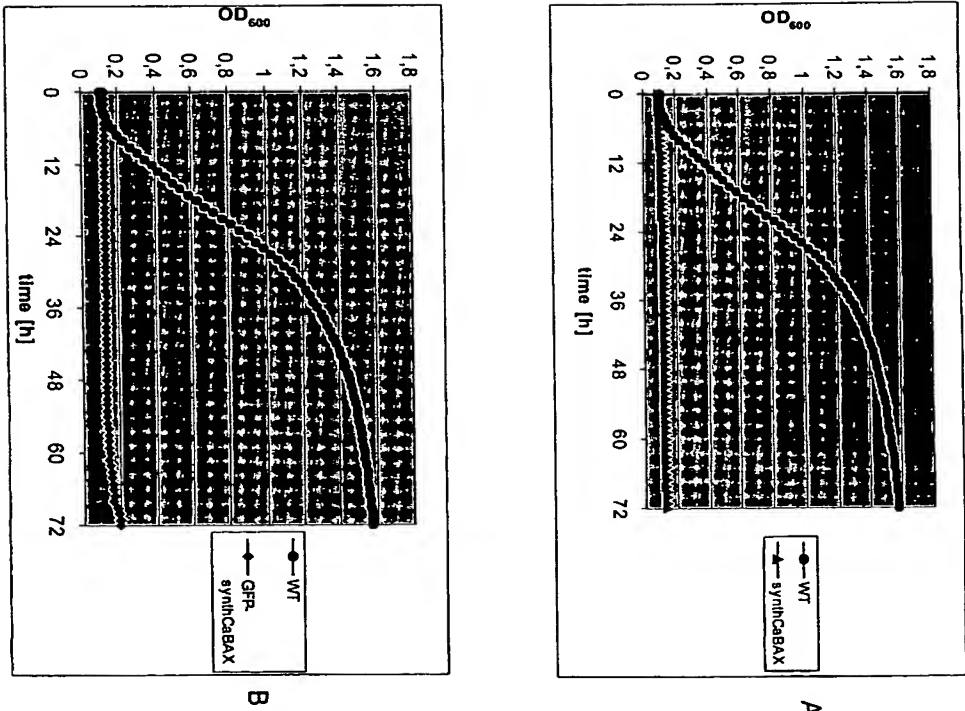


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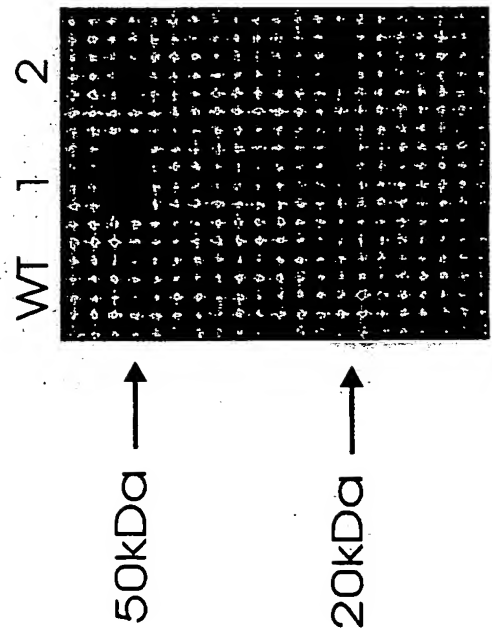


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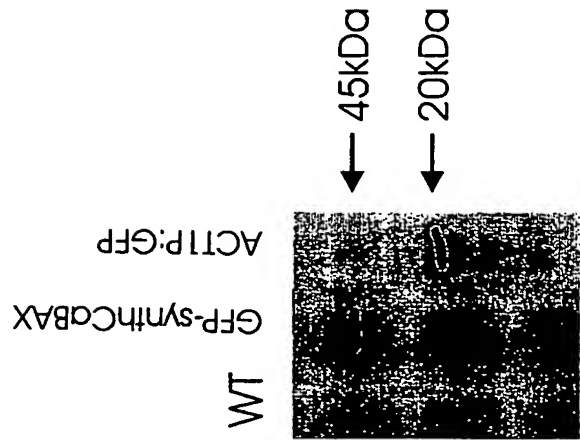


Fig. 11.

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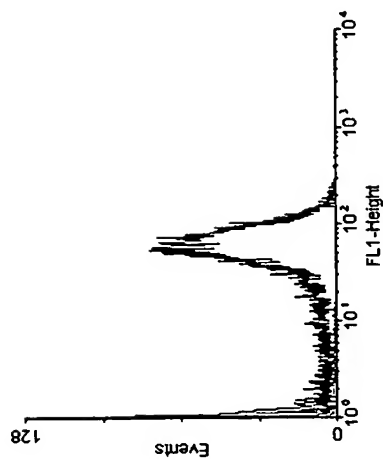
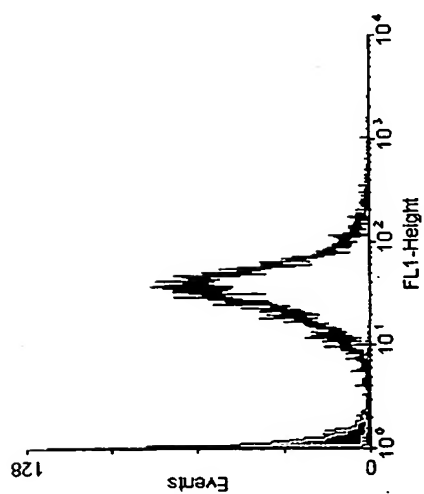


Fig.12.

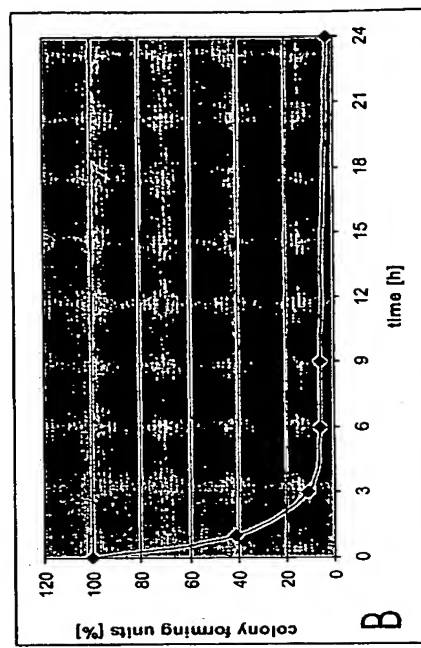
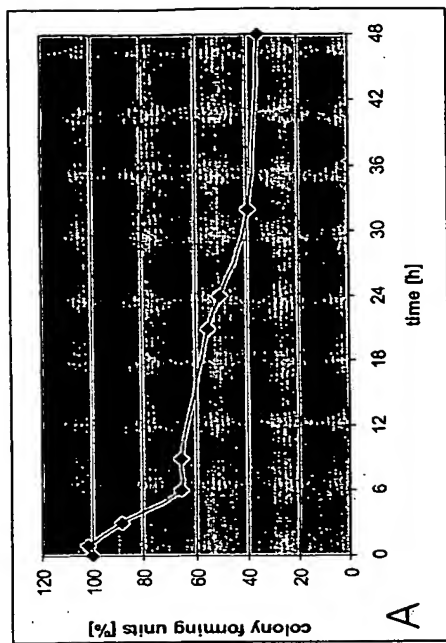


Fig. 13.

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